

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gatanaga, T.
Granger, G.A.

(ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis
Factor Receptor Releasing Enzyme Activity

(iii) NUMBER OF SEQUENCES: 154

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 PAGE MILL ROAD
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: USSN 09/081,385
(B) FILING DATE: 014-NOV-1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME:
(B) REGISTRATION NUMBER:
(C) REFERENCE/DOCKET NUMBER: 22000-20577.21

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-813-5600
(B) TELEFAX: 650-494-0792
(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTTTGT	CTTCCTTCC	CCGGAAAGG	CCGGGGCCAG	AGACCCGCAC	TCGGACCAGG	60
CGGGGGCTGC	GGGGCCAGAG	TGGGCTGGGG	AGGGCTGGGA	GGGCGTCTGG	GGCCGGCTCC	120
TCCAGGCTGG	GGGCCGCCAG	CTCCGGGAAG	GCAGTCCTGG	CCTGCGGATG	GGGCCGCCGCG	180
TGGGGCCCCG	CGGGGCCGCC	TGGGAGGGCC	TCCAGGCTGC	GGGAGGGGGA	GGAGGCCCG	240
TGGGGCGGCC	AGGGCCGTGG	GTGGAGGTGG	CCGTCCCCTC	TGAGGGGCAG	CCAGTGCGTT	300
TGGGACCCGG	GACCAAGAGCC	CGCGCCTCCC	CAGCGGCCTC	CCCGGGGGTC	TCACCGGGTC	360
ACCCGAGAGC	GGAGGGCCCCG	GCTCCGCAGA	AACCCGGGGC	GGCCGGGGGG	AAGCAGGCC	420
CTCAGGCCCTC	GGAGGAGGCC	CCAGAAAGGAC	CTCGCGCCTT	CCCGCCGGGC	TCCGACCGCC	480
TGGGTTCCGGT	GGGGGACGGC	CCAGGCCGCC	AGGACCCCCA	AGCCGAGCTC	AGCTGCGGG	540
GCACGACCCA	GAGGCCAGCA	GCAGAGGACG	GGGCGGGGGC	CGGGAGAGGG	CGGGGAGGGC	600
GCTCTGGGA	GGTCAGGGCC	AGGGCTAGAC	TTTCAGGGTC	ATGGCCTGGC	CCCTCATCCC	660
CAGGGAGGTG	AGGGGGCTCT	GTGAGCAGAG	GGGGCCCCGG	TGGAGAAGGC	GCTGCTAGCC	720

AGGGGCGGGG	CAGGAGCCCA	GGTGGGGACT	TAAGGGTGGC	TGAAGGGACC	CTCAGGCTGC	780
AGGGATAGGG	AGGGAAGCTA	GGGGTGTGGC	TTGGGGAGGT	GCTGGGGGAC	CGCGGGCGCC	840
CTTTATTCTG	AAGCCGAATG	TCCTGCCGGA	GTCCCCAGTG	ACCTAGAAAT	CCATTTCAAG	900
ATTTCAAGGA	GTTCAGGTG	GAGACAAAGG	CCAGGCCAG	GTAAAAATGT	GGCAGTGAACA	960
GAGTATGGG	TGAGAACCAAC	GGAGAGAGGA	AGTCCCCGAG	GCGGATGATG	GGACAGAGAG	1020
CGGGGACCAAG	AATTTTTAA	AACGCATCTG	AGATCGTGT	GGCAGACTCA	TAGTTGTTT	1080
CCTTCACGG	AGAAAGTGTG	GGCAGAAGCC	AGCTCTAAAG	CCCAGGCTGC	CCAGCCTGCA	1140
CTGGCAGAGC	TGACGGAAGG	CCAGGGCAGA	GCCTTCCCCTC	CCTGTCACAG	ACATGAGCCC	1200
TGGAGATCTG	GAATGAGGCA	GATGTGCCCA	GGGAAGGCTG	ATCCGCCCCC	ACCCAGGGCC	1260
CCCCGGTGC	CCCTTGAGC	GTGGAATCGT	TGCCAGGTCA	TGGCTCCCTG	CTATCGAACAA	1320
CCGGACACGG	GTGCGTGTGCT	GCACCTGGCA	GTTGCAGGAC	CGACACCCAC	AATGCCTTAA	1380
GAGGTGATGA	CTGCCTTCCA	GGGGCCTGGC	TGGCTGACAC	TTTGCATGGC	TCCTGGAGAA	1440
GAGGGATTGA	GTGGAGTCCA	CGGGTCACTG	CCACCTCTG	GGTCTGCTCT	CTGAGGGCAGG	1500
GCCCCGCTGG	GGTGAGAAGG	GGCTGGAGAC	AGGTTCTCTG	CAGTTCAACCC	TCTAACCGGT	1560
GGTCTTCATG	CCTAGGAACCC	CACTGGGGGC	TTATGAAACT	GCAGGTGGCT	GAGTCCTTGC	1620
CATGGGTCT	CTCCTTCAGG	AGGTCTGGGT	GGGGCCGGAG	ACTGACCCCC	ACAAAGGGTC	1680
CCAGGTGAGG	CGGAGTGTGGC	CTGGCGCTGT	GTGGCTCTGG	ACCTAGTCT	TGGGCTTGGG	1740
CTGGCCTCCA	GGGCCTGGGC	TTGAGACAGC	TGTGACGCA	GCAAGCCATT	TACCCCGTT	1800
GTGGGGACAT	TACATCTTCC	TAGCTTGGAA	CACACAGGCA	GCCAGGGTTG	TTATCCACAT	1860
TCCCTCTCCA	TGTTCTTC	TGAGAACATT	TTACCAAGTA	TGTCAGGAGC	TGGGCTCCAC	1920
CAGGGAGACT	CAAGTGGAAA	GGCCCTCATCC	TTGTCCTCCA	GGAGACAGGA	AAACCTATGG	1980
TTACAATTCC	AGGGACAAGA	GCGATGCTG	TGAGGTGTGG	CAAATCTCAC	TGTTCAACTG	2040
GAGAAAATCAG	AGACAGCTTC	CTGGAGGCAG	TGACACCTGG	ACAGGCTCT	CCACAGGAGG	2100
AAGCGAGTGA	GAGAACCCAA	CTGGGATGGA	CCCATCATGT	AGGGGAAACA	GTGCGCCGAG	2160
AACCAACAAAC	ACCCCCAAC	CTAGGCCAG	AGCTCACGGA	GAGAGCTGGG	CCTCTCGGGG	2220
TGACTACATA	GTTCCTCTGCT	GGATCTTAGG	TCTTGTCTT	GGGCAGCTCT	GCTGAGACCT	2280
CTATGCCTGT	TCCAGGCTGC	ACCAAGGTTT	TGTGACTATT	GGTCTGGGGT	TGTTTGCAG	2340
CAACTGAAGT	GTTCCTGTTG	AAAACAGGCA	CTTGATTGTC	TGAAAGGAAT	GCTGTTTGT	2400
CTTGCCTCGA	CAAACATTGA	GCAGCATTAA	GTGGGCGTTG	TATATCTGT	GGAGTAATGG	2460
GTGTTTTCTG	AGTCTGTCTG	GGGTACTGCA	CATTAAGG	AAATCATTT	TCTGAAACAT	2520
TGCTATTTC	CACACCGAGAA	ATCATATCCT	TTGCTGGTC	CATGTCTGAA	GACCTTACAC	2580
GAGAAAAGTCT	TAATGTAAGT	TTAGTAGAGT	CCTTGGATGG	AGAAACTAATT	ATATCATACA	2640
TTGCCGCTTT	CTCACTCTGC	TCTTTTCAT	CCTTGCCTAA	TTTCATTTC	TTCTGCTTCT	2700
TTTGTGTTCT	TCTGGAGAA	TCTAGCAAGA	TATCTGGGG	AAACATCTGA	GGTGATGAAC	2760
AAGGTAGAGA	CTGAGATTGT	AGGATTAAG	GTGGCTTG	GCCTTAAAGG	GTTCTTCAC	2820
TTCCAGCAGG	GGAGCATACT	GGCTGTGGAG	ATCTCAAGGG	AAAAGATGCA	GCATTCCTCA	2880
TTGGTGAAGG	ATCTCCATCG	TCACTACTTA	GGCTGTGCAC	CATGTGTAGG	TAGTCTTCAC	2940
TTGAACCATG	TCTAGGATTA	TCAGCATGAT	GATTAGCTGA	ATTGCCAGAC	AACGGACCAAG	3000
AAACTTTTAT	ATCATGTATG	TTTCTCAAAC	CACCTGCAAC	AATGGGACTT	GATACCGATG	3060
CTTGTGTCAT	CTGTGAGTGT	GTGTTGTAAC	TTGAAGGATG	GGAATATGGC	ATGTATCTG	3120
CAGGGCTTTG	TGGGGCGTAT	GGACTAGGCA	CTGGGTATT	TTGCTGTGGC	ATAAAATCTGT	3180
TCCCAAGAGCT	TGTCTGTGGT	GGCACAAACC	GGCTGGAGGG	GCTATGTGAG	ATAGTGGTTT	3240
GTTGATAATT	GGAAGATGCA	GGACTACTGT	GCATGGAATT	CTGAGAAAGT	TTATACTGAG	3300
ACATCATCAT	TCCACTTTGT	ACATATCTGT	TCTGTCATG	TTTCTCTCTG	AAAACATTAG	3360
GACTCTTCG	CAGGACGGCC	TGCAACAAAGA	CTGGTATGTC	ACCTTCTGGG	TCATCACTGC	3420
CAAGGTATTC	TTTCAACTCT	ATGTGATCTG	TTGATACCTG	GGTGGACCTA	TGGACAAGCT	3480
GTGAACACAA	ATTGTCATCC	CTACAAGCCA	AAAGGCAGTT	CACCTCTCT	GCTATTCTG	3540
CATTAAAGAG	AAGGCTCTT	GTAGTTGAG	CAGGTAAGG	AGATGGAAGA	GGCAGCTGGT	3600
TCAGGAGGTC	TGTGAGACTA	GCAATCCCCG	CAAGAGTAGT	AATGGGGACA	TGGGGCATAT	3660
CCCCATTCTCAT	CTCTGAATTTC	TGGAATGGTG	TTGCTCTATAA	AAGTACTTAG	TTCAGGTGCC	3720
AGCTGTCTT	ACTTCCCATT	TCCCAAAACAC	TGGGGCAATC	GGCGTCTGAA	TCCAAGGGGA	3780
GGCCGAGGCC	GCTGTGGCGA	GAGACTATAA	TCCGGGCCGG	GAGGGGGGGC	GGCTACGGCT	3840
CCTCTCCCTG	CTCCCTAGTG	CGGGGAACAT	GTAGAGCCCG	GGGGAGACCA	GCCGAGAAGA	3900
CAAATCGTTG	CTTCTCTTC	CTCCCTCTCC	TCCTTCCTCC	ACATAGAAAC	ACTCACAAAC	3960
ACCCGACCAAC	GGGGCCGAGC	TACCGGGGGG	GCATCGCCGC	GGGGCCGGGA	ACCAATTCTC	4020
CTGTCGGCGG	GGGCGTCTT	TGGATCC				4047

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGATCCAAG	GTCAAACCTCC	CCACCTGGCA	CTGCCCCGG	AGCGGGTCGC	GCCCCGGCCGG	60
CGCGCGGCCG	GGGCCCTGGC	GCCAGAAGCG	AGAGCCCCCTC	GGGGCTCGCC	CCCCCGCCTC	120
ACCCGGTCA	TGAAAAAAAC	ATCAGAGTAG	TGGTATTCTA	CCGGGGCCCG	GCAGGGCCGG	180
CGGACCCCGC	CCCCGGCCCC	TCGCGGGGAC	ACCGGGGGGG	CGCCGGGGGC	CTCCCACTTA	240

TTCTACACCT	CTCATGTCTC	TTCACCGTGC	CAGACTAGAG	TCAAGCTAA	CAGGGTCTTC	300
TTTCCCCGCT	GATTCGGCCA	AGCCC GTTCC	CTTGGCTGTG	GTTTCGCTGG	ATAGTAGGTA	360
GGGACAGTGG	GAATCTCGTT	CATCCATTCA	TGCGCGTCAC	TAATTAGATG	ACGAGGCATT	420
TGGCTACCTT	AAGAGAGTC	TAAGTTACTCC	CGCCGTTAC	CCGCGCTTCA	TTGAATTTC	480
TCACTTGAC	ATTCAAGAGCA	CTGGGCAGAA	ATCACATCGC	GTC AACACCC	GCCCGGGGCC	540
TTCGCGATGC	TTTGT TAA	TTAACACTC	GSAT TCCCCT	GGTCCGGACC	AGTTCTAAGT	600
CGGCTGCTAG	GCGCCGGCCG	AAGCGAGGCG	CCGCGCGGAA	CCGCGGCCCC	CGGGCGGGAC	660
CCGGGGGGGG	GACCGGGCCG	CGGGCCCTCC	GCCGCCTGCC	GCCGCCGCC	CCGCGCGCG	720
CCGAAGAAGA	AGGGGGAAA					739

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAAGAGTGGC	GGCCGCAGCA	GGCCCCCGG	GTGCCCCGGC	CCCCCTCGAG	GGGGACAGTG	60
CCCCCGCCCG	GGGGGGCCCG	CGGCGGGCCG	CCGCCGGGCC	CTGCCGCCCC	GACCCTTCTC	120
CCCCCGCCCG	CGCCCCCACG	CGGCGCTCCC	CCGGGGAGGG	GGGAGGACGG	GGAGCGGGGG	180
AGAGAGAGAG	AGAGAGAGGG	CGCGGGTGG	CTCGTGCCTGA	ATTCAAAAG	CTT	233

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGATCCAAG	AATTCCGGAC	GAGGTAGTCA	CGGCTCTTGT	CATTGTTGA	CTTGACGTTG	60
AGGCTGGTA	GCTTGGAAAA	GTGATGCGC	AGCGTGACG	AGGCGTTGA	GATGTTCTGC	120
CCGCTTCCAG	ACAGCTTGGC	GTGCTGGCG	CTCACGGGT	CCGCATACTG	CAGCAGGCC	180
TGGAACCTGGT	TGTTCTTGT	GAAGGTGATG	ATCTTCAACA	CTGTGCCAA	CTTGGAGAAA	240
ATCTGGTCA	GCACATCCAG	GGTCACAGGG	TAGAAGAGGT	TCTCCACGAT	GATCCTGAGC	300
ACGGGGCTCT	GCCCCGCCAT	CGCCATCCCT	GCATCCACGG	CCGCGCCGA	GGCAGGCCAAG	360
GCCAGGTCTC	CCGACTGGAC	CGAGGTTCACC	GCCTGCGAGG	CCGCCCTGGC	CCGCGCCCTGG	420
TTGGAGAGC	TGTCGGTCTT	CAGCTCCTTG	TGGTGGAGA	ACTGGATGA	GATGGGCTGG	480
CCGGCGAGCA	CAGGGGTCA	CGAGGTGTAG	TAGTTCACCA	TGGTATTGGC	AGCCTCCCTC	540
GTGTTCATCT	CGATGAAGGC	CTGGTTTTTC	CCCTTCAGCA	TCAGGAGGTT	GGTGACCTTC	600
CCAAAGGGCA	GCCCCAGGGA	GATGACTTCC	CCCTCCGTA	CGTCGATGG	GAGCTTCCGG	660
ATGTTGATCA	CTCTAGAGGG	GACGCCCTCA	CTTCGGCTG	CACCTTGA	CTTCTTGTG	720
TCATTTCCGT	TTGCTGCAGA	AGCCGAGTTG	CTGCTCATGA	TAACCGTCC	TTAGTGACA	780
CAACTAGAGA	AAAGCTCGTC	AGATCCCCG	TTTGTACCAA	CGGCTATATC	TGGGACAATG	840
CCGTCATGC	CACACAGAGC	AGACCCGGG	GGGACGGAGT	GGAGGCCGCG	GAATCCCTGA	900
GCTAGAGCTG	CAGATTGAGT	TGCTGCGTA	GACGAAGCG	AAGTATGAGA	GTGTCCTGCA	960
GCTGGGCCG	GCACACTGAC	CCCACCTTA	CAGCCTGCTG	CAGACCCAGC	ATGCACTGGG	1020
TGATGCCCTT	GCTGACCTCA	GCCAGAACGT	CCCAAGCTT	CAGGAGGAAT	TTGGCTACAA	1080
TGCAAGAGCA	CAGAAACTAC	TATGCAAGAA	TGGGAAACG	CTGCTAGGAG	CCGTGAACCT	1140
CTTTGCTCT	AGCATCAACA	CATTGGTCAC	CAAGACCATG	GAAGACACGC	TCACTGACTGT	1200
GAACACGTAT	GAGGCTGCCA	GGCTTGAATA	TGATGCCAC	CGAACAGACT	TAGAGGAGCT	1260
GAGTCTAGGC	CCCCGGGATG	CAGGGACACC	TGGTCGACTT	GAGAGTGGCC	AGGCCACTTT	1320
CCAGGCCCCAT	GCCGAGAACGT	ATGAGAACG	GGGGGGAGAT	GTGGCCATCA	AGCTCAAGTT	1380
CCTGGAAAGAA	AACAAAGATCA	AGGTGATGCA	CAAGCAGCTG	CTGCTCTTCC	ACAATGCTGT	1440
GTCGGCTTAC	TTTGCTGGGA	ACCAAGAAACA	GCTGGAGCAG	ACCCCTGCAGC	AGTTCAACAT	1500
CAAGCTGCCG	CCTCCAGGAG	CTGAGAAACC	CTCCCTGGCTA	GAGGAGCAGT	GAGCTGCTCC	1560
CAGCCCCAACT	TGCTCTTCAA	GAAGAACATT	GGGAAGGGCA	GCCCCAGGGT	GTGGGAGATT	1620
GGACATGGTA	CATCCTTGT	CACTTGGCT	TGGCTTGGG	CTCCCTTTC	TGGCTGGGGC	1680
CTGACACCAAG	TTTGCCCCAC	ATTGCTATGG	TGGGAAGAGG	GCCTGGAGGC	CCAGAACATTG	1740
CTGCCCTGTC	TATCTTCTG	GCCACAGGGC	TTCATTCCTA	GATCTTTCC	TTCCACCTCA	1800
CAGCCAACGG	CTATGACAAA	ACCACTCCCT	GGCCAATGGC	ATCACTCTC	AGGCTGGGGT	1860
GTCCTCCCTG	ACCAATGACA	GAGGCTGAAA	ATGCCCTGTC	AGCCAAATGGC	AGCTCTTCTC	1920
GGACTCCCT	GGCCCAATGA	TGTTGCGTCT	AATACCCCTT	GTCTCTTCTC	TATGCGTGCC	1980
CATTGCGAG	AAGGGACTG	GGACCAAAGG	GGTGGGGATA	ATGGGGAGCC	CCATTGCTGG	2040

CCTTGCATCT	GAATAGGCCT	ACCCTCACCA	TTTATTCACT	AATAACATTT	ATTTGTGTT	2100
TCTAATTAA	AATTACCTT	TCATCTTGCT	TGATTTCTC	TCAGCTAAAT	TAGAAATTG	2160
TAGTTTTC	CCTAAAAAAAT	TCAATGGCAT	TCTTCTTAT	AAATTACATT	CTCTGATTT	2220
CTTGTCAAGC	TGCTTCAGG	AAATCCATGT	GTCAAAATG	CTTGCTCCCA	GTTTGCTCCA	2280
TACCAAATGG	TTGCTTAACC	CAAATATCGT	AGCAGCAAAAT	TGAGCTGATC	CTTCTGGAGA	2340
AAGTACGGTT	GAACAGCCAA	GACCACTGGG	TAGTCGAAGA	GAAGACCCACA	CATCCTGAC	2400
TCCCCAGTCT	GGTGTGAGGG	GAGGACAGCT	GATAACTGGA	TATGCACTGT	TCCCAGACAT	2460
CACTGGTCCC	AAACCATTAC	TTCTGCCCTGC	CACTGCCACA	AATAACAGTAG	GAATGCCATC	2520
CCCTTCATAC	TCAGCTTAA	TCCTCAGAGT	TTCATCTGGT	CCTTATGCG	CAGATGTTAC	2580
TGGAAGTICA	CATGGATACC	CAAATTTCC	ACAGGCCCTTC	TGATTTTTT	CACAGTGACC	2640
AAGATCAGAA	GTAGAGCCCA	TCAACACTAC	AACCCCTGAC	TGACTTTCTG	ATTTAAAAG	2700
CAACTCTACT	CTCTCTGCAA	CCCACTCAA	GTTTTCTTT	ACCATTGGA	GCCCTTCAGG	2760
AGTTACTCT	TTGAGGTCCC	GATAAGACTG	TTTGCTTTTC	TGTTGGCTTC	GATCTCCTGA	2820
TGGCCAGAGT	CTCCAGGAAT	CATTGTCAT	AACATCAGCA	AGAACAAATT	CTTTGGTGGT	2880
TACATCAACA	CCAAATTCAA	TCTTCATATC	AACCACTGTA	CAATTCTGGG	GCAACCAGGA	2940
TTTCTCAGT	ATTCAAATA	TAGCCTGTG	AGCATCTCGT	GCCGAATTCA	AAAAGCTT	2998

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGCTTTTG	TGAAACACCT	AGGATATGTC	CCCTCCCTCA	CCACACCCAA	CCCCCGGCC	60
CTGCCCCAGG	ACATGACGAT	GCCTCACACA	CACACACACA	CACACATACA	CACAAGGCCG	120
TGAGCTGCAC	GCAGGAACAT	GGGCTGCACT	CACGACAACA	TTGAAAAAAT	ATACATTATA	180
TATGTACACC	CGGGGCCCCC	ACGTCCCCTC	CCGTCCCCGC	AGCCTGGCA	CACCAGGTCA	240
CGGAGGAGGG	GCCGGGGCTG	CAGGACCTCA	GGACTGCAAG	GGCAGGAAGG	AAACAGGAC	300
AAGAAAGGAA	GAAGAGTTGG	AAGGAGGGAG	AAATGGGGTC	CCCGACTGTA	AATGGAAATG	360
AGGTGGGCG	ATCATAAGAG	AAGCAGGGAC	CATGGTCCAG	CTGAGGGAGC	CCTGCAGAGG	420
GGGAAAGCT	TCCCATGGAC	AGGAGAGAGA	AGGGAAGGGG	AGAGGGAGG	GTTTCCTCA	480
ATCCCACCCC	CAGCCCCAGC	CCCAGCCCCA	GCCATTGCAA	TGTCACCCCT	CTCCCCAACAA	540
CAGTGAATGTC	TAAGGGGCA	GCTGCCATTG	GGGGTAGAAA	GGCAGCTGAA	GTCCAGCCCCA	600
CTTCCAAAC	CAGCAGGACC	CAGTGAAGG	GGCACACCG	GAGCATGACA	GCCCAGAAAGT	660
GAGGGATGGG	GGGCCCCGGG	AGGGCAAGGG	CGGACTCTCG	AGGGCCGGCT	GGGGTTTGA	720
AATGAAAGGA	GGACTGGTTC	TGAAGCCTCT	CTCCCTCTTG	GTCTCTGTG	TCCCAGAAAG	780
TCCTTCCTCC	ATGTCCTGGG	TGTCCTGTT	ACCAGGGAG	AATTCCCCCT	CTGCCTGGGG	840
AGAGGTGAG	GCCTTAGTAG	CGGTGTGGGG	GGGTCTCGAT	GATGCGCTC	TCGTCGCTG	900
TGGGGAAATC	GGCCACCTTC	GAGTCACTGC	TGTCCTCATC	CTCCTGCTGG	CCCCCAACAG	960
CCCCCGTCAC	ACAGGACTGC	CGATTCTGTT	AGGACTCTCA	GGGTTTCA	ATGATGGTGA	1020
GAGCTGAGTC	ATCCCAGAAG	AGGTCTGGGT	CCTTGGGGTC	ACTGGAGGCC	CCTGGAGGCC	1080
CGCCGGCCCC	TGAGACCGGG	CGGTGAAGGG	AATGGATGCC	CACCAAGGCC	AGGACGACCA	1140
TGAGCACCAAG	GAAGGCCAAC	CACACCAAA	TGATGAGGGT	TGGGGCGCTG	GTATCATGG	1200
AGTTCTGTG	GGAGCTGGTC	AGGCTGTGTC	AGCCCATCTC	AGGGGGGGC	TGTTGACCA	1260
GTCAGGAGG	CTGCTGGGG	CTGAGCACGT	GGCTGGGTG	GGCAACCCCG	TTCATGCTG	1320
GCAGGACATT	GACCTCCACG	ATGAATTAT	TGCTGGAGTA	ACGGCCATTC	ATTTCGAGC	1380
AGGAAAGCCG	GAACCTTCTG	GTGTAGAGGG	CAGCTCCCTG	TCGCAGGCCA	TAACGAGCT	1440
GCCTCAGGAT	CTCTTCATAC	ACAGTGTGTC	TCTCCACCCC	AGCAATAGTG	AGTAGGGAG	1500
ATGTGTTGGT	GAGCTCCAGC	CCCCCTGCT	CGAGAGAGGT	TGTCCTCAGG	AGCAGGCTTT	1560
CCCGCTCGGG	ATCCAGGTCA	TCCCTCCACCA	GAGAAATTTC	ACGGCCATTC	AGGTGTTGCA	1620
CAATCTCATC	CGACATCGCT	GTGTCGTCA	CTGTGCCCTG	CCAACCTCTCA	TCCCTTTGG	1680
CCTCCACCTG	GTGAGAAATG	GAGCAGGTGA	TTTGAAGATC	AGGGAAACAA	GGGACGCCGT	1740
TGTTCCCTC	AAAGTCCACA	GCTGGCGGG	CAAATATGAC	AGTGCACACTC	AGCAGGACT	1800
GGGGGGCGGT	AGGGCTGAGG	ACGACCACTG	AGCCCTCCAC	TTCAAGGATG	GAGACGCCAG	1860
ACTCTTCGCT	GAAGCACTTG	ACAGCAGTGG	TGAGGGCGAG	GGGCTTGACG	CCGGCCGTGG	1920
CAAAGCCAG	AGTGTTCATG	TAAGCCACAT	GCTGAGGGC	ATGGTTGAAG	GTCTCCACAT	1980
CATCCCCCTC	CAGGGTGGAC	AGGGACTGTG	AGGGGTTCAC	GTGGACCTTC	ATGCCTTTC	2040
CCAGGCTCTC	GAATCCCTA	TAGTCCAGGC	CCTCCCGACA	TGCTAGAGG	CACTCGATGA	2100
CCTCGCGGCT	CTCCAGGGCA	CCTGAGCGCA	CGCTGAAACC	AGCCAGGTAG	CCATGGAAGT	2160
AGTGTGGAT	CGACAAGGG	TCTCTTGGG	TGGTGTCTG	ACTGTTGCT	CCCTTTCT	2220
TCTCTTGTG	CTTCTCCCTA	GTCCAGCAGG	CCCCAATCAT	GAGAGCAGGC	TCCCTTCGGG	2280
GTGGGGGGAT	GAGGCCATTG	TGATGGATGA	GGGCAAGGGC	GAAGGGAGATG	CCGTCGGTAT	2340
AGAGGTGAC	TGTTGGGAAAC	TGAGGGTCA	GAGCGTAGTG	GTGCCACTCA	TCATCACAGA	2400
CCTGCTCCAG	CTTCCAGAGG	AACCTGACTG	GGCAGGGCACT	CTCAAGCAGG	GGCCAGTAGA	2460
GGAAGGCAAT	CCTACAGCCG	TGAGCAGTCA	GCGAGTAGTG	AGAGAAAGCCG	TCCTCATCT	2520
GGACAGTGT	ACATACGATG	GTTCCTCTT	CTTCTTGCC	CTTGTGGGA	GTACGCCAT	2580
GCTTCATCCA	GAAGGACAGG	GTGAAGTGGT	CACTGAGGCT	GTCCCTGGGGC	CCAGACCCCA	2640

GCCCCACTGGG	GCCACCCAGG	GGCACCTGCA	CAGCCTGGGT	GCCATTGAAC	CAGTAGATCA	2700
GGCTGCTGTC	CTGGCTGTAG	TGCACCGAGA	GTCTCTGCTGT	CCAGTTGCCA	TTGGGGCCAG	2760
GCATGGGCAA	CAGATCCACT	TCCCCAGTGG	CAGCACCACA	AGGTTCCCGC	AGCGCCCCGCT	2820
CTGAGTAGTT	GTCACGGTCA	CAGCCCTGG	CCACCATGGCT	GTCCTGCAAC	TCTATGGTGG	2880
CCTGAATGTT	CCAGAGTGGT	TCATCACAGG	TCTCCAGGCG	GATACCAGGG	AACAAAGCCA	2940
AGCTCCCAGC	ACCTGGTGCA	TATTCGATCC	TTTGTTCGA	GCCTTGCCAG	CTGGGTTTAC	3000
AGGTGGCTT	CACCTGAATC	TCCACCTCG	CATCATCTGC	TGCCCGCTTC	TTCCCACAGT	3060
CATAAGCTGT	CACTGTAAAC	TTATAGAGGC	TCTCACCACT	GTACTGCAGC	TTCTCTGTGT	3120
TCTCAATGTT	CCCGTCATTG	TCATAGGAGA	AAGGGGTGTT	GGGTGTGAGA	ATCTCATAGT	3180
AGCAGATCTG	GCTGTACTGG	GGGGGAGCAGT	CACCGTAAT	GCCTTCCACC	CGCAGGATGC	3240
GATCGTACAG	CTTCCCCCTCT	GTCACAGCGC	CACGATACAG	CCGTTCCACA	AAACACTGGGG	3300
CAAACCTGTT	CACATCGTTG	ACCCGACAT	GCACAGTGGC	CTTGTGGAC	TTCTTGGTGT	3360
TGGCCCCGTC	GGGGCCCTCG	CCACAGTCAT	AGGCTGGAT	GGTGAAGGTG	TGTTCTCTTCT	3420
GGGCTCGCA	GTCCCACAGGC	TCTTGGCCC	GGATCAGGCC	CTTCCCTGTC	GCCTTGTCAA	3480
GGATCACAGC	CTCAAAAGGC	ACCCCAAGACC	CATGGAGCGC	GAAGCCGCAG	ATCTCACCTG	3540
CATAGCGCAG	CGGGGCATCC	TTGTTCAAGG	CAAAGAGTGG	TGGATTCACTG	AGGACCGTGT	3600
TGTCAATTCTC	CATGACGATG	CCCTGGTACT	CTGCCCTAAC	CCATGGCTTG	TGCTTGTGG	3660
CTTGTGTTACA	GGAGCAGGAC	GCGAGCAGAG	AGGCCAGCAG	AAGGGGCAGC	AGCAGGAGGG	3720
TCATGGTGGC	GGCTGGGCA	GGGGCAGGCC	AGGCGTTGG	CTCCCCCTGGG	AGCCTCCAGC	3780
CTGCGGATTC	CACCTTGCAG	GAGGGATACA	GGGGGGGAAA	ACCCAAAATAA	AACGTCAAAT	3840
AAATTGTGTA	GGAGGGAGTCC	AGCTTAGGAC	CGGGCCAGAG	CCAGGCCAGG	CTCGGGGAGG	3900
GGGCCTCTGC	AGGTTCAAGG	GATCACTGCT	GCCACCAACCG	CCACCCCTGGG	AGCCAGTTAT	3960
TTTGGCATGG	CCTTGATTGC	AACAGCTGGC	TCCCTCTGTCA	TGGCAGACAG	CACCGTGATC	4020
AGGATCTCTT	CTCACACAGTC	GTACTCTGC	TCATCTCTT	TGCCAAGGTC	TCCCTCAGGG	4080
AGACGAAGGT	CCTCTCGTAC	CTCCCCGCTG	TCCCTGGAGCA	GTATAGGTA	CCCATCCTGG	4140
ATCTTTGGAT	CC					4152

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGATCCAAG	ATTCGGCACG	AGTGGCCACA	TCATGAACCT	CCAGGCCCC	CCCAAGGCTC	60
AGAACAAAGCG	GAAGCGTTGC	CTCTTTGGGG	GCCAGGAACC	AGCTCCCAAG	GAGCAGCCCC	120
CTCCCCCTGCA	GCCCCCCCCAG	CAGTCCCATCA	GAGTGAAGGA	GGAGCAGTAC	CTCGGGCACG	180
AGGGTCCAGG	AGGGGCAGTC	TCCACCTCTC	AGCCTGTGGC	ACTGGCCCCCT	CCTAGCAGCC	240
TGGCCCTGCT	GAACCTCTGT	GTGTATGGC	CTGAGCGGAC	CTCAGCAGCC	ATGCTGTCCC	300
AGCAGGGTGC	CTCAGTAAAG	TGGCCCAACT	CTGTGATGGC	TCCAGGGCGG	GGCCCGGAGC	360
GTGGAGGAGG	TGGGGGTGTC	AGTGACAGCA	GCTGGCAGCA	GCAGCCAGGC	CAGCCTCCAC	420
CCCATTCAAC	ATGGAACACTG	CACAGTCTGT	CCCTCTACAG	TGCAACCAAG	GGGAGCCCCC	480
ATCCTGGAGT	GGGAGTCCC	ACTTACTATA	ACCAACCTGA	GGCACTGAAG	CGGGAGAAAAG	540
CGGGGGGGCC	ACAGCTGGAC	CGCTATGTC	GACCAATGAT	GCCACAGAAAG	GTGAGCTGG	600
AGGTAGGGCG	GGCCCAGGCA	CCCCCTGAATT	CTTCCACAGC	AGCCAAGAAA	CCCCCAAACC	660
AGTCACTGCC	CCTGCAACCC	TTCCAGCTGG	CATTGGCCA	CCAGGTGAAC	CGGCAGGTCT	720
TCCGGCCAGG	CCCACACCC	CCAAACCCGG	TGGCTGCCTT	CCCTCCACAG	AAGCAGCAGC	780
AGCAGCAGCA	ACCACAGCAG	CAGCAGCAGC	AGCAGCAGGC	AGCCCTACCC	CAGATGCCGC	840
TCTTTGAGAA	CTTCTATTCC	ATGCCACAGC	AACCCCTCGCA	GCAACCCCGAG	GACTTTGGCC	900
TGCAGCCAGC	TGGGCCACTG	GGACAGTCCC	ACCTGGCTCA	CCACAGCATG	GCACCCCTACC	960
CCTTCCCCCC	CAACCCAGAT	ATGAACCCAG	AACTGCGAA	GGCCCTTCTG	CAGGACTCTAG	1020
CCCCCGCAGC	AGCGCTACCT	CAGGCCAGA	TCCCCCTTCC	CCGCCGCTCC	CGCCGGCTCT	1080
CTAAGGAGGG	TATCTGCCT	CCCCAGCCCC	TGGATGGGGC	TGGCAGCCCC	CCTGGGCAGG	1140
AGGCCACTGG	CAACCTGTC	CTACATCACT	GGCCCTCGCA	GGACCCGGCA	CCTGGCTCTCC	1200
TGGGGCAGCC	CCATCTGAA	GCTCTGGAT	TCCCGCTGGA	GCTGAGGGAG	TCGCAGCTAC	1260
TGCCTGATGG	GGAGAGACTA	GCACCCAATG	GCCGGGAGCG	AGAGGCTCT	GCCATGGGCA	1320
GGCAGGGAGG	CATGAGGGCA	GTGAGCACAG	GGGACTGTGG	GCAGGTGCTA	CGGGGGCGGAG	1380
TGATCCAGAG	CACGCCACGG	AGGCCGCCCC	CATCCCAGGA	GGCCAATTG	CTGACCCCTGG	1440
CCCAGAAGGC	TGTGGAGCTG	GCCTCACTGC	AGAATGAAA	GGATGGCAGT	GGTCTGAAAG	1500
AGAACCGGAA	AAAGTGTATTG	GCCTCAACTA	CCAAGTGTGG	GTTGGAGTT	TCTGAGCCTT	1560
CCTTAGCCAC	CAAGCGAGCA	CGAGAAGACA	GTGGGATGGT	ACCCCTCATC	ATCCCAGTGT	1620
CTGTGGCTGT	GCGAACGTG	GACCCAACTG	AGGCAGCCCC	GGCTGGAGGT	CTTGATGAGG	1680
ACGGGAAGGG	TCTTGAACAG	AACCCCTGTC	AGCACAAGGC	ATCAGTCATC	GTCAACCCGCA	1740
GGCGGTCCAC	CCGAATCCCC	GGGACAGATG	CTCAAGCTCA	GGCGGAGGAC	ATGAATGTCA	1800
AGTTGGAGGG	GGAGCCTTCC	GTGCGGAAAC	CAAAGCAGCG	GCCCAGGCC	GAGCCCCCTCA	1860
TCATCCCCAC	CAAGGGGGC	ACTTTCATCG	CCCCCTCCGT	CTACTCCAAAC	ATCACCCCCAT	1920
ACCAGAGGCCA	CCTGCGCTCT	CCCCGTGCC	TAGCTGACCA	CCCCCTCTGAG	CGGAGCTTTG	1980
AGCTACCTCC	CTACACGCCG	CCCCCCATCC	TCAGCCCTGT	GGGGGAAGGC	TCTGGCCCTCT	2040

ACTTCAATGC	CATCATATCA	ACCAGCACCA	TCCCTGCC	TCCTCCC	ACGCCTAAGA	2100
GTGCCCATCG	CACCGCTGCTC	CGGACTAACAA	GTGCTGAAGT	AACCCGGCCT	GTCCTCTCTG	2160
TGATGGGGGA	GGCCACCCCA	GTGAGCATCG	AGCCACGGAT	CAACGTGGG	TCCC GGTTCC	2220
AGGAGAAAAT	CCCCTTGATG	AGGGACCGTG	CCCTGGCAGC	TGAGATCCC	CACAAGGCTG	2280
ACTTGGTGTG	GCAGCCATGG	GAGGACCTAG	AGAGCAGCG	GGAGAAGCAG	AGGCAAGTGG	2340
AAGACCTGCT	GACAGCCGCC	TGCTCCAGCA	TTTCCCTGG	TGCTGGCACC	AACCAGGAGC	2400
TGGCCCTGCA	CTGTCGAC	GAATCCAGAG	AGGACATCTC	GGAAACGCTG	AATAAGCTGC	2460
TGCTGAAGAA	GCCCCGCG	CCCCACAACC	ATCCGCTGGC	AACCTATCAC	TACACAGGCT	2520
CTGACCAAGTG	GAAGATGGCC	GAGAGGAAGC	TGTTCAACAA	AGGCATTGCC	ATCTACAAAGA	2580
AGGATTCTT	CCTGGTCAG	AAAGCTGATCC	AGACCAAGAC	CGTGGCCAG	TGCGTGGAGT	2640
TCTACTACAC	CTACAGAAAG	CAGGTAAAAA	TGGGCCGCAA	TGGGACTCTA	ACCTTTGGGG	2700
ATGTGGATAC	GAGGCGATG	AAGTCGGCCC	AGGAAGAGGT	TGAAGTGGAT	ATTAAGACTT	2760
CCAAAAGTT	CCCCAAGGTG	CCTCTTCCA	GAAGAGAGTC	CCCAAGTGA	GAGAGGCTGG	2820
AGCCCAAGAG	GGAGGTGAAG	GAGGCCAGGA	AGGAGGGGA	GGAGGAGGTG	CCAGAGATCC	2880
AAGAGAAGGA	GGAGCAGGAA	GAGGGGCGAG	AGCGCAGCG	CGGGCAGCG	GCAGTCAAAG	2940
CCACGCAGAC	ACTACAGGCC	AATGAGTCGG	CCAGTGACAT	CCTCATCCTC	CGGAGCCACG	3000
AGTCCAACGC	CCCTGGGTCT	GCCGGTGGCC	AGGCCTCGGA	GAAGCCAAGG	GAAGGGACAG	3060
GGAAGTCACG	AAGGGCACTA	CCTTTTCAG	AAAAAAAAAA	AAAAAAACAA	AAAGCTT	3117

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCCGCA	CGAGGTCACT	TTCTCTGTGGA	ACACAGAGGC	TGCGCTGTCCC	ATTCAGACAA	60
CGACGGATAC	AGACCAGGCT	TGCTCTATAA	GGGATCCCAA	CACTGGGATT	GTGTTAAC	120
TTAATCCGCT	AAACAGTTCG	CAAGGTATATA	ACGTCTCTGG	CATTGGGAAG	ATTTTTATGT	180
TTAATGTCG	CGGCACAATG	CCTGTCGTCG	GGACCATCCT	GGGAAACCT	GCTTCTGGCT	240
GTGAGGCCAGA	AACCCAAACT	GAAGAGCTCA	AGAATTGGA	GCCAGCAAGG	CCAGTCGAA	300
TTGAGAAAAAG	CCTCCAGCTG	TCCACAGAGG	GCTTCATCAC	TCTGACCTAC	AAAGGGCCTC	360
TCTCTGCCAA	AGGTACCGCT	GATGCTTTA	TGTCCTGGCTT	TGTTGCAAT	GATGATGTTT	420
ACTCAGGCC	CCTCAAAATC	CTGCATCAAG	ATATCGACTC	TGGCGAGGG	ATCCGAAACA	480
CTTACTTGA	GTTTAAACC	GCCTTGGCCT	GTGTTCCCTC	TCCAGTGGAC	TGCCAAGTCA	540
CCGACCTGGC	TGGAATGAG	TACGACCTGA	CTGGCCTAA	CACAGTCAGG	AAACCTTGG	600
CGGCTGTTG	CACCTCTGTC	GATGGGAGAA	AGAGGACTTT	CTATTTGAGC	GTTTGCAATC	660
CTCTCCCTTA	CATTCTGGG	TGCCAGGGCA	GGCGAGTGGG	GCTTGTCTTA	GTGTCAGAAG	720
GCAATAGCTG	GAATCTGGGT	GTGGTGCGA	TGAGTCCCCA	AGCCGCGCCG	AACTGGATCTT	780
TGAGCATCAT	GTATGTCAC	GGTACAAGT	GTGGGAACCA	GCGCTTCTCC	ACCAGGATCA	840
CGTTTGTAGT	TGCTCAGATA	TCGGGCTCAC	CAGCATTCA	GTTCAGGAT	GTTGTGAGT	900
ACGTGTTAT	CTGGAAACT	GTGGAACCT	GTCGGCTGT	CAGAGTGGAA	GGGGACAAC	960
GTGAGGTGAA	AGACCCAAGG	CTGGCAACT	TGATGACCT	GAAGGCCCCG	GGCCTCAACG	1020
ACACCATCGT	GAGCGCTGGC	GAATACACTT	ATTACTTCG	GGTCTGTGGG	AACTTTCTC	1080
CAGACGCTG	CCCCACAAGT	GACAAGTCCA	AGGTGGCTC	CTCATGTCAG	AAAAAGCGGG	1140
AACCCGAGGG	ATTCACAAA	GTGGCAGGT	TCCCTGACTCA	GAAGCTAAT	TATGAAAATG	1200
GCTTGTAA	AATGAACCT	ACGGGGGGGG	ACACTTGC	TAAGGTTTAT	CAGCGCTCCA	1260
CAGCCATCTT	CTTCTACTGT	GACCGCGGCA	CCCAGCGGCC	AGTATTTCTA	AAGGAGACTT	1320
CAGATGGTC	CTACTGTGTT	GAGTGGCGAA	CCCGTAGATGC	CTGCCACCT	TTCGATCTGA	1380
CTGAATGTT	ATTCACAAAGT	GGGGCTGGCA	ACTCTTCGA	CCTCTCGTCC	CTGTCAGGT	1440
ACAGTGACAA	CTGGGAAGCC	ATCACTGGG	CGGGGGACCC	GGAGCACTAC	CTCATCAATG	1500
TCTGCAAGTC	TCTGCCCTCC	CAGGCTGGCA	TGAGGCTGTG	CCCTCCAGAA	GCAGCCGCCG	1560
GTCTGCTGGG	TGGCTTAAGG	CCCGTAGGAA	TGGCAGGGCC	AAGGGACGGA	CCTCAGTGG	1620
GAGATGGCAT	AATTGCTCTG	AAATACGTTG	ATGGCGACTT	ATGTCAGAT	GGGATTCGGA	1680
AAAAGCAAC	CACCATCCGA	TTCACCTGCA	GCGAGAGCCA	AGTGAACCTC	AGGCCCATGT	1740
TCATCAAGCGC	CGTGGAGGAC	TGTGAGTACA	CCTTGTCCCTG	GCCCCACAGCC	ACAGCCTGTC	1800
CCATGAAGAG	CAACGAGCAT	GATGACTGCC	AGGTCAACAA	CCCAAGCACA	GGACACCTGT	1860
TTGATCTGAG	CTCCCTTAAGT	GGCAGGGCGG	GATTCAACAGC	TGCTTACAGC	GAGAAGGGGT	1920
TGGTTACAT	GAGCATCTGT	GGGGGAGAATG	AAAATGCCC	TCTCTGGCTG	GGGGCCTGCT	1980
TTGGACAGAC	CAGGATTAGC	GTGGGCAAGG	CCAACAAGAG	GCTGAGATAC	GTGGACCAGG	2040
TCCTGCACTG	GGTGTACAAG	GATGGGGTCC	CTTGTCCCTC	CAAATCCGC	CTGAGCTATA	2100
AGAGTGTGAT	CAGTTCTGTC	TGCAAGGCC	AGGCGGGGCC	AACCAATAGG	CCCATGCTCA	2160
TCTCTCTGGA	CAAGCAGACA	TGCACTCTCT	TCTCTCTG	GCACACGCC	CTGGCCTGCC	2220
AGCAACCGAC	CGAATGTTCC	GTGAGGAATG	GAAGCTCTAT	TGTTGACTTG	TCTCCCCCTTA	2280
TTCATCGCAC	TGGTGGTTAT	GAGGCTTATG	ATGAGAGTGA	GGATGATGCC	TCCGATACCA	2340
ACCCGTGATT	CTACATCAAT	ATTGTCAGC	CACTAAATCC	CATGCACCGA	GTGCCCTGTC	2400
CTGCCGGAGC	CGCTGTGTGC	AAAGTTCTA	TTGATGGTCC	CCCCATAGAT	ATCGGCCGGG	2460
TAGCAGGACCC	ACCAATACTC	AATCCAATAG	CAAATGAGAT	TACTTGAAT	TTTGAAAGCA	2520

GTACTCCTTG	CCAGGAAATT	AGTTGTAAT	AAAATTGAAC	CTGCTCAACA	GCTGAGGGAG	2580
ACTAGAAATG	ATGGGTCCAT	ATCCTGGTGC	ATTGTCATAC	AATTCAAACA	ATGGTGCAGC	2640
TACCAGCTTG	TAATTTTAG	GGACTGAAA	CAAGGCTTT	TCTTGAAGCT	GAACCAGAAA	2700
CAACCTCTTA	TGTTCTTAG	GCTTGTAAAT	ATGTCAGGA	ATATATGGAT	ACTGAGGAGG	2760
TTCAAAATT	GGTCTCCACC	AGTTACCAAT	GCAATCGTCA	ATGACCCAGT	CTTGCAAAAC	2820
TCCATCCTGA	CGACCCAGTA	TCTCTGTCA	TAAGCGTTT	AGTCCTCAA	CTTCATCTTC	2880
TCCTGGGTTA	AGTTACCCAC	CAGGTAGTT	GAAGAAAGT	GTTCCCAGCT	GCACGAGTAA	2940
CACATGGGGT	AGCCGGTGCT	CATGTACAAAT	CAGAACCCCT	TCTACAGTCC	TCCTCATTC	3000
AATTATCA	AATTCTTCCC	TCATGCCGTG	AAATCTGGCT	GCAACAGAGC	TGTCCTTCTC	3060
GTAGAGGGGC	TCTTTTGTAC	CAAAGATA	ATTGGTAAGA	GGGTACAGGT	TGATGGTGG	3120
CTCCAGGGTG	AGGGGCTTCG	TCTGCTGGAT	GTACTTGTG	CCGAACGTGAG	TGACCCCCCG	3180
GGGCCAGCCG	GTCTGGAGC	GATTGGCGG	TACACAGAC	ATGCTGGCGA	GCTCCGGCGC	3240
TGACGGCGAG	CAGAAAGTGG	CAGGCAGGGT	AGACTTTCCC	CGTGCAGGAA	GCCTCGTGC	3300
GAATTC						3306

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCCGCA	CGAGAATGGA	TCAACCTCAA	CAACACGTTA	AAAGCTAGACG	AAAGAAGTAA	60
TACACAGTGT	ATGAGCTCA	CATGAAATAC	CCGGATGTAA	ATCCAAAGAA	ACAGGAAGCA	120
GATTGGGGT	TGCCAGGGAC	AAGGGCGGTG	GGAGGAGAAA	ATGGAGAGTA	ACGGGACTTT	180
ACTTTGGAG	TGATGAGAAT	GTTTGGAGC	TAGATAGAAG	TGGTGGTTGT	ACACCATTGT	240
GGATGTACTA	CCACTTAATT	GTTCACTAA	AAATTTAATT	TATGTGAATT	GCATCTTAAT	300
TAAAAAACAG	GATAAACATTC	CAACTCCTGG	ACATTATCCT	TCTTCTTCAT	TTGATGTCAG	360
GCCCCGTTA	GAATTCTCAT	CGCGTTGGT	CACTGCACTT	AAAGATGTGGA	GAATTTAGGA	420
CGCACAGGTA	AGAGGAAGGA	TAACACTGAT	TAAGGTAGTG	CTTTCTTAGG	TTTCCCCCAA	480
ACAATTTAAC	AGATGGATAG	TGGCACCACT	TACCGAGATGG	AAAAACCCAGC	GGAAAGGAAGA	540
TTTGGGGGAG	AAGTTAACGT	TGTCTTGGC	CTGTGTTTG	CAACCTGAGT	GTAAAAGACA	600
TATGTTAACG	CTTCAGTGGC	GAAACACTAA	AACAGAAAT	GGATCAGAAAT	TTTATCTTTG	660
GATGTGACTT	CTCAAGGATG	GCTTGTCA	TTCAGTGCCT	GTCAAATGA	CAAGATGGGC	720
AATCTTTTC	TGAAGGTCCA	AGCACCTGAA	CGTGGCAGGG	TGACCCGATT	CCGATTGCT	780
TAGAACAAATC	CTAGTTCATG	CCTATTGTCC	CTCATGTAAT	TAATATCACT	CTCAAAATGT	840
CTCATTGTTG	GCAAAATTAAT	CTGCAACGTT	ATGGCGCGAC	TCTCGCGGCC	CGAGCGGCC	900
GACCTTGCT	TCGAGGAAGA	GGACCTCCC	TATGAGGAGG	AAATCATGCC	GAACCAATTG	960
TCTGCAAT	GCTGGCTCA	CTACATCGAG	TTCAAACAGG	GCCCCCGGAA	GCCCCAGGCTC	1020
AATCAGCTAT	ACGAGCGG	ACTCAAGCTG	CTGCCCTGCA	GCTACAAACT	CTGGTACCGA	1080
TACCTGAAGG	CGCGTCGGGC	ACAGGTGAAG	CATCGCTGTG	TGACCGACCC	TGCGCTATGAA	1140
GATGTCAACA	ACTGTCTATG	GAGGGCCTT	GTGTCATGC	ACAAGATGCC	TCGCTGTGG	1200
CTGATTACT	GCCAGTTCC	CATGAGCC	GGCGCGCTGA	CACACACCCG	CCGCACCTTC	1260
GACCGTCCC	TCCGGGCACT	CCCCATCACG	CAGCACTCTC	GAATTTCGCC	CCTGTATCTG	1320
CGCTTCTGC	GCTCACACCC	ACTGCCCTGAG	ACAGCTGTG	GAGGCTATCG	GGCGCTTCTC	1380
AAGCTGAGTC	CTGAGAGTGC	AGAGGAGTAC	ATTGAGTACC	TCAAGTCAAG	TGACCGCTG	1440
GATGAGGCCG	CCCAGGCCCT	GGCCACCGTG	GTGAAACGACG	AGCGTTTCGT	GTCTAAGGCC	1500
GGCAAGTCCA	ACTACCAGT	GTGGCACG	CTGTGCGACC	TCTATCTCCA	GAATCCGGAC	1560
AAGGTACAGT	CCCTCAATGT	GGACGCCATC	ATCCGGGGGG	GGCTCACCCG	CTTCACCGAC	1620
CAGCTGGCA	AGCTCTGGT	TTCTCTGCC	GACTACTACA	TCCGCAGCGG	CCATTTCGAG	1680
AAGGCTCGGG	ACGTGTACGA	GGAGGCCATC	CGGACAGTGA	TGACCGTGC	GGACTTCACA	1740
CAGGTGTTG	ACAGCTACGC	CCAGTCCAG	GAGAGCATGA	TGCTGTGAA	GATGGAGACC	1800
GCCTCGGAGC	TGGGGCGCGA	GGGAGGAGAT	GATGTGGACC	TGGAGCTGCC	CCTGGCCCGC	1860
TTCGAGCACG	TCATCGACG	CGGGCCCTG	CTCTCAACA	GGCTCTTGT	GGCCAAAAAC	1920
CCACACCAAG	TGCACCGAGT	GCACAAAGCT	GTGCCCTCTG	ACCGAGGCCG	CCCCGGGGAG	1980
ATCATCAACA	CCTACACAGA	GGCTGTGCG	ACGGTGGACC	CCTTCAGGC	CACAGGCAAG	2040
CCCCACACTC	TGTGGGTGGC	GTTTGCAAG	TTTATGAGG	ACAACGGACA	GCTGGACGAT	2100
GCCCCGTGTC	TCCTGGAGAA	GGCCACCAAG	GTGAACTTCA	AGCAGGTTGGA	TGACCTGGCA	2160
AGCGTGTGGT	GTCAGTGGG	AGAGCTGGAG	CTCCGACACG	AGAACTACGA	TGAGGCC	2220
CGGCTGCTG	GAAAGGCCAC	GGCGCTGCC	GGCCGCCGGG	CCGAGTACTT	TGATGGTCA	2280
GAGCCCGTGC	AGAACCCGCT	GTACAAGTC	CTGAAGGTCT	GGTCCATGCT	CGCCGACCTG	2340
GAGGAGAGCC	TCGGCACCTT	CCAGTCCACC	AAAGCCCGTGT	ACGACCGCAT	CCTGGACCTG	2400
CGTATCGCAA	CACCCAGAT	CGTCATCAAC	TATGCCATGT	TCTTGGAGGA	GCACAAGTAC	2460
TTCGAGGAGA	GCTTCAGGAC	TCAGCAGCGC	GGCATCTCGC	TGTTCAAGTG	GCCCCAACGTG	2520
TCCGACATCT	GGAGCACCTA	CCTGACCAAA	TTTATTGCC	GGCTATGGGGG	CCGCAAGCTG	2580
GAGCGGGCAC	GGGACCTGTT	TGAACAGGCT	CTGGACGGCT	GGCCCCC	ATATGCCAAG	2640
ACCTTGTAAC	TGCTGTACGC	ACAGCTGGAG	GAGGAGTGGG	GGCTGGCCCG	GCAATGCCATG	2700
GCCGTGTAAC	AGCGTGCAC	CAGGGCCGTG	GAGCCCCCCC	AGCAGTATGA	CATGTTCAAC	2760

ATCTACATCA	AGCGGGCGGC	CGAGATCTAT	GGGGTCACCC	ACACCCGCGG	CATCTACCAG	2820
AAGGCCATTG	AGGTGCTGTC	GGACGAGCAC	GCGCGTGAGA	TGTGCTGCG	GTGGCAGAC	2880
ATGGAGTCA	AGCTCGGGGA	GATTGACCGC	GCCCCGGCCA	TCTACAGCTT	CTGCTCCCAG	2940
ATCTGTGACC	CCCGGACGAC	CGGGCGTTG	TGGCAGACGT	GGAAGGACTT	TGAGGTCGG	3000
CATGGCAATG	AGGACACCAT	CAAGGAAATG	CTGCGTATCC	GGCGCAGCGT	GCAGGCCACG	3060
TACAACACGC	AGGTCAACTT	CATGGCCTCG	CACATGCTCA	AGGTCTCGG	CAGTGCCACG	3120
GGCACCGTGT	CTGACCTGGC	CCCTGGGAG	AGTGGCATGG	ACGACATGAA	GCTGCTGGAA	3180
CAGCAGGCGAG	AGCAGCTGGC	GGCTGAGGCG	GAGCGTGACCC	AGGCCCTGGC	CGCCAGAGC	3240
AAGATCTGT	TCTGAGGAG	TGACGCCCTC	CGGGAGGAGC	TGGCAGAGCT	GGCACAGCAG	3300
GTCAACCCCG	AGGAGATCCA	GCTGGCGAG	GACGGAGGAGC	AGGACGAGAT	GGACCTGGAG	3360
CCCAACGAGG	TTCGGCTGGA	GCACGAGAGC	GTGCCAGCGC	CAGTGTGTTG	GAGCCTGAAG	3420
GAAGACTGAC	CCGTCCTCC	GTGCGAATT	CGGCACGAGC	AAGACCAAGCC	CCCAGATCAT	3480
TTGCCTCAA	GGTTTCCCT	CGAATCACA	AATGTTTCAA	GGAATCTCAA	ATTTTACAAA	3540
GTGTTGAAGT	TGGGATATTG	TGGGCTGTGG	TCTGTCTTC	TCTCTGTAGC	TGTTTTCTCC	3600
CTACATCCC	GAAAGGAAGT	TGACGCTGCT	CCCTCCATCCG	CAGACCTCCC	TTTCCAGCGC	3660
CCAGGGCATG	GGGTGCTGTG	AGGGCAGCAT	GCTAGGTGTG	ACCGTGTCTC	TGGCCTCCAG	3720
GCCCCTGTC	CTCTGTCTC	TAGCCACTA	AGGCCCTGGC	CCATTGTGC	TAAACAGGCA	3780
GTCGGACCTA	GAAAGAGCAG	ACAATCTCTC	TGGGTACCA	GTCTGGCTAG	GAGCTGGTCT	3840
CCTGACTGGG	ATCCAGGCT	TCTCCCTGC	CCATGTGAAT	TCCCAGGGGC	AGAGCCTGAA	3900
ATGTTGAACA	CAGCACTGGC	CAAAGAGATG	TCACCGTGGG	AACCGAGGCT	CTCTTCTCC	3960
CCTGCCTGCT	TTCTGGGTT	CAGAGTAGCT	GAGGCTTGTC	TGAGAGGAGT	TGGAGTGTG	4020
GTGTTCAACC	TGGTTGGTGT	GCTTGCTTT	GAGGGCACTT	AGAAAGCCCA	GCCCAAGCCCT	4080
TGCTCCCTGCC	CTGCAACACAG	CGGAGCAGCT	TTCTAGGTA	TGCTCTTGAT	TTCTGAGAA	4140
GCAGCAGGTG	GCATGGAGGC	AAGAGGAAGT	GTGACTGAAA	CTGTCCACTC	ATAGCCGGC	4200
TGCCGTATTG	AGAGGGCT					4218

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGCTCGGGC	GCCTCGAGGT	CGACACTAGT	GGATCCAAAG	AATTGGCAC	GAGGGAAACT	60
CAACGGGTGA	CGAGTGGAGG	ACAGGGACAG	AGGCCCTCTGT	GGTGGAACGA	CCCCACCTCG	120
AGGAGCTTCC	TGAGCAGGTG	GCAGAAAGATG	CGATTGACTG	GGGGCAGCTT	GGGGTAGAGG	180
CACTGCTCTG	GGGGACTGAC	TCTGGCATCT	CTGCCGAGGC	TGCTGGAATC	GACTGGGCA	240
TCTTCCCGGA	ATCAGATTC	AAGGATCTG	TGGGTGATGG	GATAACTG	GGAGACGATG	300
CTGTTGCTT	CGAGATCACA	TGCTGGAAG	CAGGAAACCC	GGCTCCAGAA	GGTGTGCCA	360
GGGGCCAGA	TGCCCTGACA	CTGCTGAAAT	ACACTGAGAC	CCGGAAATCAG	TTCCCTGATG	420
AGCTCATGGA	GCTTGGAGTC	TTCTTAGCCC	AGAGAGCAGT	GGAGTTGAGT	GAGGAGGAG	480
ATGTCCTGTC	TGTGAGCCG	TTCCAGCTGG	CTCCAGCCAT	CCTGAGGGC	CAGACCAAAG	540
AGAAGATGGT	TACCATGGTG	TCAGTGCTGG	AGGATCTGAT	TGGCAAGCTT	ACCACTTTC	600
AGCTGCAACA	CCTGTTATG	ATCTGGCCT	CCACCAAGGT	TGTGGACCGA	GTGACTGAAT	660
TCCCTCAGCA	AAAGCTGAAG	CAGTCCCGAG	TGCTGGCTTT	GAAGAAAGAG	CTGATGGTGC	720
AGAAGCAGCA	GGAGGCACTT	GAGGAGCAGG	CGGCTCTGGA	GCCTAAAGCTG	GACCTGCTAC	780
TGGAGAAGAC	CAAGGAGCTG	CAGAAGCTGA	TTGAAGCTGA	CATCTCAAG	AGGTACAGCG	840
GGCGCCCTGT	GAACCTGTG	GGAACTCTC	TGTGACACCC	TCCGTGTTCT	TGCCCTGCCCA	900
TCTTCTCCG	TTTGGGATG	AAGATGATAG	CCAGGGCTGT	TGTTTGGGG	CCCTCAAGG	960
CAAAAGACCA	GGCTGACTGG	AAGATGGAAA	GGCACAGGAA	GGAAAGGGCA	CCTGATGGTG	1020
ATCTTGGCAC	TCTCCATGTT	CTCTACAAAGA	AGCTGTTG	ATTGGCCCTG	TGGTCTATCA	1080
GGCGAAAACC	ACAGATTCTC	CTTCTAGTTA	GTATAGCGCA	AAAAGCTCT	CGAGAGTACT	1140
TCTAGAGCGG	CCCGGGGCC	ATCGATTTTC	CACCCGGGTG	GGGTAC		1187

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCTCACTAA	AGGAAACAAA	AGCTGGAGCT	CGCGCGCTG	CAGGTGACCA	CTAGTGGATC	60
GAAAGTTCTG	TACGCGAACG	TGAAATTAA	CTCTGGCTG	ACCCATAAAC	ATTGTCTGA	120

TCTAGGATAT	AGTTGCCTT	CTTGCGGGCA	GCAATCTGGA	TGAGGCCTGTT	GAGGCACTGG	180
GTGGCCTGCT	GGATCAGGAC	ATCCCAGCGG	CCAGCATAGT	TCCGCTGCCG	GCGTAGGCC	240
ATCACCCGCA	TCTTATCCAT	GATGGCATTG	GTACCCAGGA	TGTTGTACTT	CTTGGAAAGGG	300
TTGGAGGCTG	CATGTTGAT	GGCCCATGTG	GTCTTGCAG	CAGCAGGCAG	GCCCACCATC	360
ATCAGAATCT	CACATTCCTG	CTTGTCTTT	GGTCCAACGG	TGCCCCGGAT	ACGCTCACTA	420
AGGGGAAGGT	GCTGGATGAA	GGTAACCCCC	GGGAGGACAG	AACACTAGGG	CTCTGCTCTC	480
TGTCCGAAGT	TGAACCTCCAC	TGGCAATT	TTACCCAGGA	CATGAGGATA	GAGGGCCTGA	540
CCCCCCAAAGG	CTTCTCTTG	GATTGGAAA	GCAATGCCCA	TCCACTTCC	ATTCTTGGTA	600
AAAGACATTG	CCACGTATT	TCCACATTCA	AAATCCGCAA	AGCAGGCAAT	CACCGGAGAG	660
CTCTGGGTG	CTAGGAGAGC	GGCTGGGCC	GCAGACTGGG	GGGAAAGCTC	CGCAGCGCA	720
GTGGGCCCA	GGATCAGGCC	CCGGTGGCC	TGAGAAGGCC	CAGTCTGGC	TGGAGCGGGA	780
GCTGGACAGT	GTGGCCTTG	TTCCGCCCCC	GGGAGCGCTG	CGAGTGTGCG	GGCCTCGGGT	840
GGATTGCTG	AGCACCAATA	CCTCACGGT	GCAACCTGG	GGTTTTAGCT	CCCTTGGTTT	900
TAATCCCCA	GGGGGGGTG	GGGGCACGGG	GGAAAGGATE	GGCCAGCTGG	GTGCAATCCT	960
GCTGTAAGCC	AGCCATTCTT	TGATTTCTTA	GAATTAAC	GATGGCTGCG	CCGGAGGCCG	1020
CGGGGGCCCG	AGCGGAGCAG	CCCGGCTGA	GGTCCCAG	TGCGCCGCTC	GGGGCTGCGC	1080
TCCGCCCCCG	GGACCCCGGC	CTCTGGCCGC	GGCCGCTCCG	GGCTCCGGGG	GGGCCGGGGC	1140
CGCCGGGACA	TGGTGCCTAGT	CGCACCCCTT	CCCCCGCCGC	GCTGAGCTCG	CCGGCCGGCGC	1200
CCGGGCTGG	ACGTCGGAGC	GGGAAGATGT	TTCCTCCCT	GAAGAAGCTG	GTGGGGTGC	1260
ACCAGGGCCC	GGGGGGGGC	AAGAACATCC	CCGGGGGCG	GCAGTCCATG	AACCAGGCGT	1320
TGCAGAGGCC	CTTCGCCAAG	GGGGTGCAGT	ACAACATGAA	GATGTTGATC	CGGGGAGACA	1380
GGAACACGGG	CAAGACAGCG	CTGTGGCACC	GCTGCAAGGG	CCGGCGTTC	TGGAAGGAGT	1440
ACATCCACAC	ACAGGAGATC	CAAGTCACCA	GCATCCACTG	GAGCTACAAG	ACCACGGATG	1500
ACATCGTAA	GGTTGAAGTC	TGGGATGTAG	TGACAAAGG	AAAATGCAA	AAGCGAGGCC	1560
ACGGCTTAA	GATGGAGAAC	GACCCCGAG	AGNCGGAGTC	TGAAATGGCC	CTGGATGCTG	1620
AGTTCTGGA	CGTGTACAA	AACTGCAACG	GGGTTGGTCA	GATGTTGAC	ATTACAAGC	1680
AGTGGACCTT	CAATTACATT	CTCCGGAGC	TTCCAAAAGT	GCCCACCCAC	GTGCCAGTGT	1740
GCGTGTCTGG	GAACATACCGG	GACATGGCG	AGACCCGAGT	CATCTGCG	GACGACGTGC	1800
GTACTTCTAT	CGACACCTG	GACAGACCTC	CAGGTTCCCT	CTACTTCCG	TATGCTGAGT	1860
CTTCATGAA	GAACAGCTTC	GGCCCTAAAGT	ACCTTCATAA	GTTCTCAAT	ATCCCCATT	1920
TGCAGCTTC	GAGGGAGACG	CTGTTGCGC	AGCTGGAGAC	GAACAGCTG	GACATGGACG	1980
CCACGCTGGA	GGAGCTGTG	GTGAGCGAG	AGACGGAGGA	CCAGAACTAC	GGCATCTTC	2040
TGGAGATGAT	GGAGGCTCG	AGCCGTGGCC	ATGCGTCCCC	ACTGGCGGCC	AACGGGCAGA	2100
CCCCATCCCC	GGGCTCCCG	TCACCACTC	TGCTGCGACC	CGCTGTGTC	ACGGGGAGCT	2160
CCAGCCCCG	CACACCCCG	CCCCCCCG	AGCTGCCCC	CAATGTC	CCACCATCCT	2220
CTGTGCCCC	TGTACCA	TCAGAGGCC	TGCCCCCACC	TGCGTGC	TCAGCCCCG	2280
CCCCACGGCG	CAGCATCATC	TCTAGGCTGT	TTGGGACGTC	ACCTGCCACC	GAGGCAGCCC	2340
CTCCACCTCC	AGAGCAGTC	CCGGCGCAC	AGGGCCAGC	AACGTCAG	AGTGTGGAGG	2400
ACTTTGTC	TGACGACCCG	CTGACCGCA	GTCTCTGGA	AGACACAA	CCCGCCAGGG	2460
ACGAGAAGAA	GGTGGGGCC	AAGCGTCCC	AGCAGGACAG	TGACAGTGT	GGGGAGGCC	2520
TGGGCGCAA	CCCGATGGTG	GCAGGGTTC	AGGACGATGT	GGACCTCGAA	GACCAACAC	2580
GTGGGAGTCC	CCCGCTGCT	GCAGGCC	TCCCCAGTC	AGACATCACT	CTTTCGAGTG	2640
AGGAGAAGC	AGAACATGGCA	GCTCCCACAA	AAAGCCCTGC	CCCAGCTCCC	CAGCACTGCT	2700
CAGAGCCAGA	GACCAAGTGG	TCTCCATAC	CGCTTCGAA	GGCACGGAG	GGGACAGCTC	2760
CCACGAGGC	CGCAGCACCC	CCCTGGCCAG	CGGGTGTCT	TGTCGCA	GGTCCGGAGA	2820
AGCGCAGCAG	CACCAAGGCC	CCTGCTGAGA	TGAGGCCGG	GAAGGGTGA	CAGGCTCTC	2880
CGTCGGAGAG	TGACCCGAG	GGACCCATTG	CTGCACAAAT	GCTGCTCTC	GTATGGATG	2940
ACCCCGACTT	TGAGAGCGAG	GGATCAGACA	CAACAGCGAG	GGCGGATGAC	TTTCCCGTGC	3000
GAGATGACCC	CTCCGATGTG	ACTGACGAGG	ATGAGGGCCC	TGCGGAGCCG	CCCCCACCCC	3060
CCAAAGCTCC	TCTCCCGCC	TTCAGACTGA	AGAATGACTC	GGACCTCTC	GGGCTGGGC	3120
TGGAGGAGGC	CGGACCCAAG	GAGAGCAGTG	AGGAAGGTA	GGAGGGCAA	ACCCCTCTA	3180
AGGAGAAGAA	AAAAAAACA	AAAAGCTTCT	CGAGAGTACT	TCTAGAGCGG	CCGCGGGCC	3240
ATCGATTTC	CACCGGGTG	GGTACCA	TAATGTC	CAATTGCGCC	TATAGTGAGT	3300
CGTATT						3306

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCAGGGCCA GAGTGGGCTG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAGTCCTGG CCTGCCGGATG

20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGACAGGA GAATTGGTTC

20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCCTGGGTTC GGTGCGGGAC

20

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTCTTCGGT CTCCCTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGATTGCTAG TCTCACAGAC

20

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTAAGGGTGG CTGAAGGGAC

20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACCTTCCTTC CCTGTACAG

20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACACCATTCC AGAAATTCA

20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAACTGCAGG TGGCTGAGTC

20

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCCTAATGT TTTCAAGGGAG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAAACCTATG GTTACAATTG

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCCTAGACAT GGTTCAAGTG

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATAATTA GTTCTCCATC

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCCTGTTC CAGGCTGCAC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGACGGCGAC CTCCACCCAC

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGCTCCTCC GACGCCCTGAG

20

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGTCTAGCCC TGGCCTTGAC

20

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCACTGGGG ACTCCGGCAG

20

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGCTTTCCC TGGGCACATG

20

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CACAGCTGTC TCAAGCCAG

20

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACTGTTCCCC CTACATGATG

20

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATCATATCCT CTTGCTGGTC

20

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTTCCCAGAG CTTGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTTTGGCAGA CTCATAGTTG

20

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAGCAGGGAG CCATGACCTG

20

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTTGGCCCA GAAGCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCTCTCTCTC TCTCTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCCCCGGTGA TTCCGCCAAG

20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTTTGAAAT TCGGCACGAG

20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCCTGGTCC GCACCAAGTC

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAGAAGGGTC GGGGCGGCAG

20

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AAATCACATC GCGTCAACAC

20

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAGAGAGTC ATAGTTACTC

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCTCTAGAAC TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTCTGGCCA TCAGGAGATC

20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGCCGTGT AGATGTTCTG

20

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGTGGCAGGC AGAAGTAATG

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGTTGGAGAA CTGGATGTAG

20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTATTCAAGT GCAACGCCAG

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCATGGCACA CAGAGCAGAC

20

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCTACCATGC AGAGACACAG

20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGGCTGACA AGAAAATCAG

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCACCGATA GAGGAGAGAC

20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGGGTGATGC CTTTGCTGAC

20

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAAACAAGAT CAAGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTGCCAACAT TGCTATGGT

20

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACCAAGATC AGAAGTAGAG

20

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCCTGGGCC AATGATGTTG

20

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TCTTCCCCACC ATAGCAATG

19

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGGTCTTGGT GACCAATGTG

20

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACACCTCGGT GACCCCTGTG

20

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTCCAAGTT CGGCACAGTG

20

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACATGGGCTG CACTCACGAC

20

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCCTCTGA ACCTGCAGAG

20

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGAAATGAGG TGGGGCGATC

20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTTGCCTTG GACAAGGATG

20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCACCTGCCA TTGGGGGTAG

20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGTGGAAAGCC ATTGACGGTG

20

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGCGTCTCTC GTCGCTGCTG

20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCGGAAACTC TGTGGTGCTG

20

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGGATTGCCT TCCTCTACTG

20

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTCTGTTTC ACCAGGGCAG

20

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCAGTGCCTC TATGCATGTC

20

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AGGAAGCCCA CGCACACCCAC

20

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CCCTTTGTTTC CCTGATCTTC

20

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGCTCGGGAT CCAGGTCA

20

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCGAGGTTCA GAGCGTAGTG

20

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCTTGGATCT CTGGCACCTC

20

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCATCAGAGT GAAGGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCATCTTCCA CTGGTCAGAG

20

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CTCCTTCTCT TGGATCTCTG

20

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTACTTCAGC ACTGTTAGTC

20

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AGGGAGGTAG CTCAAAGCTC

20

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TGGGTCCACA GTTCCACAG

20

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAACTCTGTG ATGGCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCAGGGTTC TGTTCAAGAC

20

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CCATTGGGTG CTAGTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CAGCCATGCT GTCCCAGCAG

20

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGGACCTGA GGTAGCGCTG

20

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATAACCACCC TGAGGCAGTG

20

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCTGCAGGTC GACACTAGTG

20

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AATTGGAATG AGGAGGACTG

20

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCTCTAGAAG TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATTGTATGAC AATGCACCAAG

20

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TCCACAGAGG GCTTCATCAC

20

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CCTGACTGGC CTAAGCACAG

20

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AAGCCTCATCA ACCACCACTG

20

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGTCAACCGT GACAAGTGTG

20

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTGTACACCA GCTGCAGGTC

20

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGGTGTGGTG CAGATGAGTC

20

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATCACACTCT TATAAGCTAG

20

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGGGAAGCT TTCCTCAGAC

20

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGATGAACAT GGGCCTGGAG

20

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATTGTGGAT GTACTACCA

20

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGTGTTTGC AACCTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATAGTGGCAC CACTTACGAG

20

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AATTCTGCAA CGTGATGGCG

20

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CACAAAGATGC CTCGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AATCCGGACA AGGTACAGTC

20

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCACGAGCTGG CACAAGCCGTG

20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCAAGCGTGT GGTGTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TGTTTGAAACA GGCTCTGGAC

20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CGGCATGGCA ATGAGGACAC

20

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGGACGAGAT GGACCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CCCTCTGTCC TCTAGCCCCAC

20

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TCTTGAGGGG ACTGACTCTG

20

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TGAGTGAGGA GGCAGATGTC

20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGGCTTGAA GAAAGAGCTG

20

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAAAAGACC AGGCTGACTG

20

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGCAGCTCCT TGGTCTTCTC

20

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATTACAGT CCCAAGGCTC

20

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATCTGGATGA GGCGGTTGAG

20

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGTCACTCTC CGACGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCCAAAG TTCGTCTCTG

20

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CGCTGTGTGT CTGATCCCTC

20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATGAAGGTAACCCCCGGGAG

20

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGGTCTCTGG CTCTGAGCAC

20

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCTGGAGAA GCCCAGTC

20

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CACACTCTGG ACCGTTGCTG

20

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAAGCTCCGC AGCCCGAGTG

20

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TCTTCCAGGA AGCTGCGGTC

20

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GATGGTGGGG CAGCATTGAG

20

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTCACCAAGTG GTGCCTGCAG

20

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACCTCACCGT TGCCAACCTG

20

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGCAACAGCG TCTCCCTCTG

20

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

AGTACCTTCA TAAGTTCTTC

20

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TCCCAGACTT CAACCTTCAC

20

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AAACATCTTC CCGGTCGGAC

20

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCTGAGCACCC TTTACCTCAC

20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GACGTCCGTC CGGGAAAGATG

20

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACACAGGAGA TGCAGGTCAC

20

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAGTCTCCA TGAAGAACAG

20

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GCAGTGAGGA AGGTAAGGAG

20

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 378...1799
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGATCCAAAG GACGCCCCCG CCGACAGGAG AATTGGTCC CGGGCCCCCG GCGATGCC	60
CCCGGTAGCT CGGGCCCGTG GTCGGGTGT TGTGAGTGT TCTATGTGGG AGAAGGAGGA	120
GGAGGAGGAA GAAGAACAA CGATTTGTCT TCTCGGCTGG TCTCCCCCG GCTCTACATG	180
TTCCCGCAC TGAGGAGACG AAAGAGGAGC CGTAGGCCGC CCCCTCCCG GCCGGATT	240
TAGTCTCTCG CCACAGCGGC CTCCGGCTCC CCTTGGGATTC AGACGCCGAT TCGCCCAGTG	300
TTGGGAAAT GGGAGTAAT GACAGCTGGC AGCTGAACTA AGTACTTTA TAGGCAACAC	360
CATTCCAGAA ATTCAAG ATG AAT GGG GAT ATG CCC CAT GTC CCC ATT ACT	410
Met Asn Gly Asp Met Pro His Val Pro Ile Thr	
1 5 10	
ACT CTT GCG GGG ATT GCT AGT CTC ACA GAC CTC CTG AAC CAG CTG CCT	458
Thr Leu Ala Gly Ile Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro	
15 20 25	
CTT CCA TCT CCT TTA CCT GCT ACA ACT ACA AAG AGC CTT CTC TTT AAT	506
Leu Pro Ser Pro Leu Pro Ala Thr Thr Lys Ser Leu Leu Phe Asn	
30 35 40	
GCA CGA ATA GCA GAA GAG GTG AAC TGC CTT TTG GCT TGT AGG GAT GAC	554
Ala Arg Ile Ala Glu Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp	
45 50 55	
AAT TTG GTT TCA CAG CTT GTC CAT AGC CTC AAC CAG GTA TCA ACA GAT	602
Asn Leu Val Ser Gln Leu Val His Ser Leu Asn Gln Val Ser Thr Asp	
60 65 70 75	
CAC ATA GAG TTG AAA GAT AAC CTT GGC AGT GAT GAC CCA GAA GGT GAC	650
His Ile Glu Leu Lys Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp	
80 85 90	
ATA CCA GTC TTG TTG CAG GCC GTC CTG GCA AGG AGT CCT AAT GTT TTC	698
Ile Pro Val Leu Leu Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe	
95 100 105	
AGG GAG AAA AGC ATG CAG AAC AGA TAT GTA CAA AGT GGA ATG ATG ATG	746
Arg Glu Lys Ser Met Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met	
110 115 120	
TCT CAG TAT AAA CTT TCT CAG AAT TCC ATG CAC AGT AGT CCT GCA TCT	794
Ser Gln Tyr Lys Leu Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser	
125 130 135	
TCC AAT TAT CAA CAA ACC ACT ATC TCA CAT AGC CCC TCC AGC CGG TTT	842
Ser Asn Tyr Gln Gln Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe	
140 145 150 155	
GTG CCA CCA CAG ACA AGC TCT GGG AAC AGA TTT ATG CCA CAG CAA AAT	890
Val Pro Pro Gln Thr Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn	
160 165 170	
AGC CCA GTG CCT AGT CCA TAC GCC CCA CAA AGC CCT GCA GGA TAC ATG	938
Ser Pro Val Pro Ser Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met	
175 180 185	
CCA TAT TCC CAT CCT TCA AGT TAC ACA ACA CAT CCA CAG ATG CAA CAA	986
Pro Tyr Ser His Pro Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln	
190 195 200	

GCA TCG GTA TCA AGT CCC ATT GTT GCA GGT GGT TTG AGA AAC ATA CAT Ala Ser Val Ser Ser Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His 205 210 215	1034
GAT AAT AAA GTT TCT GGT CCG TTG TCT GGC AAT TCA GCT AAT CAT CAT Asp Asn Lys Val Ser Gly Pro Leu Ser Gly Asn Ser Ala Asn His His 220 225 230 235	1082
GCT GAT AAT CCT AGA CAT GGT TCA AGT GAG GAC TAC CTA CAC ATG GTG Ala Asp Asn Pro Arg His Gly Ser Ser Glu Asp Tyr Leu His Met Val 240 245 250	1130
CAC AGG CTA AGT AGT GAC GAT GGA GAT TCT TCA ACA ATG AGG AAT GCT His Arg Leu Ser Ser Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala 255 260 265	1178
GCA TCT TTT CCC TTG AGA TCT CCA CAG CCA GTA TGC TCC CCT GCT GGA Ala Ser Phe Pro Leu Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly 270 275 280	1226
AGT GAA GGA ACT CCT AAA GGC TCA AGA CCA CCT TTA ATC CTA CAA TCT Ser Glu Gly Thr Pro Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser 285 290 295	1274
CAG TCT CTA CCT TGT TCA TCA CCT CGA GAT GTT CCA CCA GAT ATC TTG Gln Ser Leu Pro Cys Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu 300 305 310 315	1322
CTA GAT TCT CCA GAA AGA AAA CAA AAG AAG CAG AAG AAA ATG AAA TTA Leu Asp Ser Pro Glu Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu 320 325 330	1370
GGC AAG GAT GAA AAA GAG CAG AGT GAG AAA GCG GCA ATG TAT GAT ATA Gly Lys Asp Glu Lys Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile 335 340 345	1418
ATT AGT TCT CCA TCC AAG GAC TCT ACT AAA CTT ACA TTA AGA CTT TCT Ile Ser Ser Pro Ser Lys Asp Ser Thr Lys Leu Thr Pro Leu Arg Leu Ser 350 355 360	1466
CGT GTA AGG TCT TCA GAC ATG GAC CAG CAA GAG GAT ATG ATT TCT GGT Arg Val Arg Ser Ser Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly 365 370 375	1514
GTG GAA AAT AGC AAT GTT TCA GAA AAT GAT ATT CCT TTT AAT GTG CAG Val Glu Asn Ser Asn Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln 380 385 390 395	1562
TAC CCA GGA CAG ACT TCA AAA ACA CCC ATT ACT CCA CAA GAT ATA AAC Tyr Pro Gly Gln Thr Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn 400 405 410	1610
CGC CCA CTA AAT GCT GCT CAA TGT TTG TCG CAG CAA GAA CAA ACA GCA Arg Pro Leu Asn Ala Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala 415 420 425	1658
TTC CTT CCA GCA AAT CAA GTG CCT GTT TTA CAA CAG AAC ACT TCA GTT Phe Leu Pro Ala Asn Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val 430 435 440	1706
GCT GCA AAA CAA CCC CAG ACC AAT AGT CAC AAA ACC TTG GTG CAG CCT Ala Ala Lys Gln Pro Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro 445 450 455	1754
GGA ACA GGC ATA GAG GTC TCA GCA GAG CTG CCC AAG GAC AAG ACC TAAGA Gly Thr Gly Ile Glu Val Ser Ala Glu Leu Pro Lys Asp Lys Thr 460 465 470	1804
TCCAGCAGGG AACTATGTAG TCACCCCGAG AGGCCAGCT CTCTCCGTGA GCTCTGGGCC TAGGGTGGGG GTGGTTGTTG GTTCTGCGCG CACTGTTCCC CCTACATGAT GGGTCCATCC CAGTTGGCTT CTCTCACTCC CTTCCTCTG TGGAGAAGCC TGTCCAGGTG TCACTGCCTC CAGGAAGCTG TCTCTGATTTC TCCAGTTGA ACAGTGAGAT TTGCCAACACC TCACATGCAT CGCTCTTGTGTC CCTGGATTG TAACCATAGG TTTTCTGTGTC TCCTGGAGGA CAAGGATGAG	1864 1924 1984 2044 2104

GGCTTCCAC	TTGAGTC	CTGGTGGAGC	CCAGCTCCTG	ACATACCTG	TAAAAGTTCT	2164
CAAGAGAAGA	ACATGGAGGA	GAATGTGGA	TAACAACCC	GGCTGCCTGT	GTGTTCCAAG	2224
CTAGGAAGAT	GTAATGTCCC	CACAAACGGG	GTAATGGCT	TGCCCTGCCTC	ACAGCTGTCT	2284
CAAGGCCAGG	CCCTGGCCG	CAGCCCAAGC	CCAAGGACTA	GTCAGCAGAGC	CACACAGGCC	2344
CAGGCCACAT	CCGCTCAC	TGGGACCTT	TGTGGGTAC	AGTCTCCGGC	CCCACCCAGA	2404
CCTCCTGAAG	GAGAGACCC	ATGCAAGGA	CTCACCCACC	TGCAAGTTCA	TAAGCCCCA	2464
GTGGGTTCT	AGGCATGAAG	ACCAACGGTT	AGAGGCTGAA	CTGGCAGGAA	CCTGTCTCCA	2524
GCCCCCTCTC	ACCCCAGCCG	GGCCCTGCCT	CAGAGGCAGC	ACCCAGGACG	TGGCCATGAC	2584
CCGTGGACT	CACTCAATCC	CTCTTCTCCA	GGAGGCATGC	AAAGTGTCA	CCAGCCAGGC	2644
CCCTGGAAAG	CACTCATCAC	CTCTTAAGGC	ATTGTGGGTG	TGCCCTCTGC	AACTGCCAGG	2704
TGCAGCACAC	GACCGCTGTC	CGGTGTTCGA	TAGCAGGGAG	CCATGACCTG	GCAACGATTC	2764
CACGCTCAA	GGGGCACCCC	GGGGCCCTG	GTCAGGGCG	GATCAGCTT	CCCTGGGCAC	2824
ATCTGCTCA	TTCCAGATCT	CCAGGGCTCA	TGTCTGTGAC	AGGGAGGGAA	GGCTCTGCC	2884
TGGCCTTCG	TCAGCTCTGC	CACTGCAGGC	TGGGCAAGCT	GGGCTTATA	GCTGGCTTCT	2944
GCCCCACTT	TCTCCGTGAA	AGGAAACCAA	CTATGAGCT	GCCAAACGCA	TCTCAGATGC	3004
GTTTTAAAAA	ATTCTGGTCC	CCGCTCTCTG	TCCCATCATC	CCCTCTGGGG	ACTTCTCTC	3064
TCCGTGGTTC	TCACCCATA	CTCTGTCACT	GCCACATTT	CACCTGGGC	TGGCCTTTGT	3124
CTCCACCTGA	AACCTCTGAA	AATCTTGAAA	TGGATTTCTA	GGTCACTGGG	GACTCCGGCA	3184
GCACATTCGG	CTTCAGAATA	AAGGGCCCCC	GGGGTCCCCC	AGCACCTCCC	CAAGCCACAC	3244
CCCTAGCTTC	CCTCCCTAC	CCTGCAGCCT	GGGGGTCCCC	TCAGCCACCC	TAAAGTCCCC	3304
ACCTGGCTC	CTGCCCCG	CTTGGCTAGC	ACGGCCCTCT	CCACCGGGGC	CCCTCTGCT	3364
CACAGAGCCC	CCTCACCTCC	CTGGGGATGA	GGGGCCAGGC	CATGACCTG	AAAGTCTAGC	3424
CCTGGCCTG	ACCTCCCAGG	AGGCCCTCC	CCGCCCTCTC	CCGGCCCCGG	CCCGGTCC	3484
TGCTGCTGGC	CTCTGGTCTG	TGCCCGCAG	ACTGAGETGC	GCTTGGGGGT	CCTGGCGGCC	3544
TGGGGCGTCC	CGCAGCGAAC	CCAGGCGGTG	GGAGCCCCGG	GGGAAGGGCGC	GAGGTCCTTC	3604
TGGGGGCTCC	TCCGACGCT	GAGGGCGCTG	CTTCCCCCGG	GCCGCCCCGG	GTTTCTGCGG	3664
AGCCCCGGCC	TCCGCTCTCG	GGTGACCCGG	TGAGACCCCC	GGGGAGGGCG	CTGGGGAGGC	3724
CGGGGCTCTG	CTCCCGGGTC	CCAAACGAC	TGGCTGCC	TCAGGAGGGA	CGGCGACCTC	3784
CACCCACGGC	GCTGGCGCC	GCACGGCCGC	TCCCTCCGCT	CCCGCAGCCT	GGACGGCTCC	3844
CGAGGGCGCC	CCGGCGGCC	CCACGCGCG	CCCATCCGC	AGGCCAGGAC	TGCCCTCCCG	3904
GAGCTGGCGG	CCCCCAGCCT	GGAGGAGCCG	GGCCCGAGACG	CCCTCCCAGC	CTCCCCAGC	3964
CCACTCTGGC	CCCCCAGCCC	CCCCCTGGTC	CGAGTGC	TGGCTGCC	CGGCCTTCC	4024
CGGGGAAGGA	AAGCAAAAG	CTT				4047

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met Asn Gly Asp Met Pro His Val Pro Ile Thr Thr Leu Ala Gly Ile
 1 5 10 15
 Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro Leu Pro Ser Pro Leu
 20 25 30
 Pro Ala Thr Thr Thr Lys Ser Leu Leu Phe Asn Ala Arg Ile Ala Glu
 35 40 45
 Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp Asn Leu Val Ser Gln
 50 55 60
 Leu Val His Ser Leu Asn Gln Val Ser Thr Asp His Ile Glu Leu Lys
 65 70 75 80
 Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp Ile Pro Val Leu Leu
 85 90 95
 Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe Arg Glu Lys Ser Met
 100 105 110
 Gln Asn Arg Tyr Val Gln Ser Gly Met Met Ser Gln Tyr Lys Leu
 115 120 125
 Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser Ser Asn Tyr Gln Gln
 130 135 140
 Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe Val Pro Pro Gln Thr
 145 150 155 160
 Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn Ser Pro Val Pro Ser
 165 170 175
 Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met Pro Tyr Ser His Pro
 180 185 190
 Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln Ala Ser Val Ser Ser
 195 200 205

Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His Asp Asn Lys Val Ser
 210 215 220
 Gly Pro Leu Ser Gly Asn Ser Ala Asn His His Ala Asp Asn Pro Arg
 225 230 235 240
 His Gly Ser Ser Glu Asp Tyr Leu His Met Val His Arg Leu Ser Ser
 245 250 255
 Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala Ala Ser Phe Pro Leu
 260 265 270
 Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly Ser Glu Gly Thr Pro
 275 280 285
 Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser Gln Ser Leu Pro Cys
 290 295 300
 Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu Leu Asp Ser Pro Glu
 305 310 315 320
 Arg Lys Gln Lys Gln Lys Lys Met Lys Leu Gly Lys Asp Glu Lys
 325 330 335
 Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile Ile Ser Ser Pro Ser
 340 345 350
 Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser Arg Val Arg Ser Ser
 355 360 365
 Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly Val Glu Asn Ser Asn
 370 375 380
 Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln Tyr Pro Gly Gln Thr
 385 390 395 400
 Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn Arg Pro Leu Asn Ala
 405 410 415
 Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala Phe Leu Pro Ala Asn
 420 425 430
 Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val Ala Ala Lys Gln Pro
 435 440 445
 Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro Gly Thr Gly Ile Glu
 450 455 460
 Val Ser Ala Glu Leu Pro Lys Asp Lys Thr
 465 470

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 26...799
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

AAGCTTTTG AATTGGCAC GAGAT GCT ACA CAG GCT ATA TTT GAA ATA CTG	52
Ala Thr Gln Ala Ile Phe Glu Ile Leu	
1 5	
GAG AAA TCC TGG TTG CCC CAG AAT TGT ACA CTG GTT GAT ATG AAG ATT	100
Glu Lys Ser Trp Leu Pro Gln Asn Cys Thr Leu Val Asp Met Lys Ile	
10 15 20 25	
GAA TTT GGT GTT GAT GTA ACC ACC AAA GAA ATT GTT CTT GCT GAT GTT	148
Glu Phe Gly Val Asp Val Thr Thr Lys Glu Ile Val Leu Ala Asp Val	
30 35 40	
ATT GAC AAT GAT TCC TGG AGA CTC TGG CCA TCA GGA GAT CGA AGC CAA	196
Ile Asp Asn Asp Ser Trp Arg Leu Trp Pro Ser Gly Asp Arg Ser Gln	
45 50 55	
CAG AAA GAC AAA CAG TCT TAT CGG GAC CTC AAA GAA GTA ACT CCT GAA	244
Gln Lys Asp Lys Gln Ser Tyr Arg Asp Leu Lys Glu Val Thr Pro Glu	
60 65 70	
GGG CTC CAA ATG GTA AAG AAA AAC TTT GAG TGG GTT GCA GAG AGA GTA	292

Gly Leu Gln Met Val Lys Lys Asn Phe Glu Trp Val Ala Glu Arg Val			
75	80	85	
GAG TTG CTT TTG AAA TCA GAA AGT CAG TGC AGG GTT GTA GTG TTG ATG			340
Glu Leu Leu Leu Lys Ser Glu Ser Gln Cys Arg Val Val Val Leu Met			
90	95	100	105
GGC TCT ACT TCT GAT CTT GGT CAC TGT GAA AAA ATC AAG AAG GCC TGT			388
Gly Ser Thr Ser Asp Leu Gly His Cys Glu Lys Ile Lys Lys Ala Cys			
110	115	120	
GGA AAT TTT GGC ATT CCA TGT GAA CTT CGA GTA ACA TCT GCG CAT AAA			436
Gly Asn Phe Gly Ile Pro Cys Glu Leu Arg Val Thr Ser Ala His Lys			
125	130	135	
GGA CCA GAT GAA ACT CTG AGG ATT AAA GCT GAG TAT GAA GGG GAT GGC			484
Gly Pro Asp Glu Thr Leu Arg Ile Lys Ala Glu Tyr Glu Gly Asp Gly			
140	145	150	
ATT CCT ACT GTA TTT GTG GCA GTG GCA GGC AGA AGT AAT GGT TTG GGA			532
Ile Pro Thr Val Phe Val Ala Val Ala Gly Arg Ser Asn Gly Leu Gly			
155	160	165	
CCA GTG ATG TCT GGG AAC ACT GCA TAT CCA GTT ATC AGC TGT CCT CCC			580
Pro Val Met Ser Gly Asn Thr Ala Tyr Pro Val Ile Ser Cys Pro Pro			
170	175	180	185
CTC ACA CCA GAC TGG GGA GTT CAG GAT GTG TGG TCT TCT CTT CGA CTA			628
Leu Thr Pro Asp Trp Gly Val Gln Asp Val Trp Ser Ser Leu Arg Leu			
190	195	200	
CCC AGT GGT CTT GGC TGT TCA ACC GTA CTT TCT CCA GAA GGA TCA GCT			676
Pro Ser Gly Leu Gly Cys Ser Thr Val Leu Ser Pro Glu Gly Ser Ala			
205	210	215	
CAA TTT GCT GCT CAG ATA TTT GGG TTA AGC AAC CAT TTG GTA TGG AGC			724
Gln Phe Ala Ala Gln Ile Phe Gly Leu Ser Asn His Leu Val Trp Ser			
220	225	230	
AAA CTG CGA GCA AGC ATT TTG AAC ACA TGG ATT TCC TTG AAG CAG GCT			772
Lys Leu Arg Ala Ser Ile Leu Asn Thr Trp Ile Ser Leu Lys Gln Ala			
235	240	245	
GAC AAG AAA ATC AGA GAA TGT AAT TTA TAAGAAAGAA TGCCATTGAA TTTTTTA			826
Asp Lys Lys Ile Arg Glu Cys Asn Leu			
250	255		
GGGGAAAAAC TACAAATTTC TAATTTAGCT GAAGGAAAAT CAAGCAAGAT GAAAAGGTAA			886
TTTTAAATTA GAGAACACAA ATAAAATGTA TTAGTGAATA ATAGGTGAGG GTAGGCCAT			946
TCAGATGCAA GGCCAGCAAT GGGGCTCCCC ATTATCCCCA CCCCCTTGGT CCCAGTCCCC			1006
TTCTCTGCAA TGGGCACGCA TAGAGGAGAG ACAAAAGGGTA TTAGACGCAA CATCATGGC			1066
CCAGGGGAGT CCGAGAAAGAG CTGGCATTGG CTGACAGGGC ATTTTCAGGC TCTGTCATTG			1126
GTCAGGGAGC ACACCCCGAC CTGAGAGTG ATGCCATTGG CCAGGGAGTG GTTTGTCAT			1186
AGCCGTTGCG TGTGAAGTGG AAGGAAAAAGA TCTGGAAATG AGCCCTGTG GCCAGGAAGA			1246
TAGACAGGGC AGCAACTTCT GGGCCTCCAG GCCCCCTTCCC CACCATAGCA ATGTGGCAA			1306
AACTGGTGTG AGGCCCCAGC CAGAAAAAAGG AGCCCAAGGCC AGAGGGCAAG TGACAAAGGA			1366
TGTACCATGT CCAATCTCCC ACACCTGGG GCTGCCCTTC CCAATGTCTT TCTTGATAGC			1426
CAAGTTGGGC TGGGAGCAGC TCACGTCTCC TCAAGTCAGG CATATTCCAG AGCTCCTGG			1486
GGCCGCTAGCT TGATGTTGAA CTGCTGCAGG GTCTGCTCCA GCTGTTCTG GTTCCCAGCA			1546
AAGTAGGGGG ACACAGCATT GTGGAAGAGC AGCACGCTGT TGTCATCAC CTTGATCTTG			1606
TTTTCTTCCA GGAACCTTGAG CTTGATGGCC ACATCTCCCC GCAGCTTCTC ATACTGTCC			1666
CGATGGGCCT GGAAGATGGC CTGGGCACTC TCAAGTCGAC CACGTGTCCC TGCATCCCG			1726
GGGCCTAGAC TCAGCTCTC TAAGTCTGTT CGTAGGGCAT CATATTCCAG CCTGGCAGCC			1786
TCATACTGT TCACAGTCAT GAGCCGTGTCT TCCATGGCT TGTTGACCAA TGTGTTGATG			1846
CTAGAGACAA AGAAGTTCAC GGCTCTAGC AGCCTTCCC CATTCTGCA TAGTAGTTTC			1906
TGTGTCTCTG CATTGTTAGCC AAATTCCTCC TGAAGCTCTG GGGACTTCTG GCTGAGGTCA			1966
GCAAAGGCAT CACCCAGTGC ATGCTGGGTG TGCAAGCAGGC TGAGAGGTG GGCTGTCAGT			2026
GCCCCGGCCA GCTGCAGGAC ACTCTCATAC TTGCGCTTCC TCTCACGCAG CAACTCAATC			2086
TGCACTCTA GCTCCAGGAT TCCGGCGCCCT CCACCTCCGTC CCCCCGGGGT CTGCTCTGTG			2146
TGCCATGGAC GCCATTGTC CAGATATAGC CGTTGGTACA AAGCGGGGAT CTGACCGAGCT			2206
TTTCTCTACT TGTGTCACTA ACGGACCCTT TATCATGAGC AGCAACTCGG CTTCTGCAGC			2266
AAACGGAAAT GACAGCAAGA AGTCAAAGG TGACAGCCGA AGTGCAGGGCG TCCCCCTCTAG			2326
AGTGATCCAC ATCCGGAAGC TCCCCATCGA CGTCACGGAG GGGGAAGTCA TCTCCCTGGG			2386

GCTGCCCTT	GGGAAGGTCA	CCAACCTCCT	GATGCTGAAG	GGGAAAAACC	AGGCCTTCAT	2446
CGAGATGAAC	ACGGAGGAGG	CTGCCAATAC	CATGGTGAAC	TACTACACCT	CGGTGACCCC	2506
TGTGCTGCCG	GGCCAGCCCA	TCTACATCCA	GTCTCCAAC	CACAAGGAGC	TGAAGACCGA	2566
CAGCTCTCCC	AACCAGGGCG	GGGGCCAGGC	GGCCCTGCAG	CGGGTGAACT	CGGTCCAGTC	2626
GGGGAACTTG	GCCTTGGCTG	CCTCGCGGCG	GGCCCTGGAT	GCAGGGATGG	CGATGGCCGG	2686
GCAGAGCCCC	GTGCTCAGGA	TCATCGTGGA	GAACCTCTTC	TACCCGTGTA	CCCTGGATGT	2746
GCTGCACCAG	ATTTCTCCA	AGTTCGGCAC	AGTGTGAAG	ATCATCACCT	TCACCAAGAA	2806
CAACCAGTTC	CAGGCCCTGC	TGCACTATGC	GGACCCCGTG	AGCGCCCAAGC	ACGCCAAGCT	2866
GTGGCTGGAC	GGGCAGAACCA	TCTACAACGC	CTGCTGCACG	CTGCGCATCG	ACTTTCCAA	2926
GCTCACCAAGC	CTCAACGTCA	AGTACAACAA	TGACAAGAGC	CGTGACTACC	TCGTGCCGAA	2986
TTCTTGGAT CC						2998

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

Ala Thr Gln Ala Ile Phe Glu Ile Leu Glu Ser Trp Leu Pro Gln
 1      5          10        15
Asn Cys Thr Leu Val Asp Met Lys Ile Glu Phe Gly Val Asp Val Thr
 20     25          30
Thr Lys Glu Ile Val Leu Ala Asp Val Ile Asp Asn Asp Ser Trp Arg
 35     40          45
Leu Trp Pro Ser Gly Asp Arg Ser Gln Gln Lys Asp Lys Gln Ser Tyr
 50     55          60
Arg Asp Leu Lys Glu Val Thr Pro Glu Gly Leu Gln Met Val Lys Lys
 65     70          75        80
Asn Phe Glu Trp Val Ala Glu Arg Val Glu Leu Leu Leu Lys Ser Glu
 85     90          95
Ser Gln Cys Arg Val Val Val Leu Met Gly Ser Thr Ser Asp Leu Gly
100    105         110
His Cys Glu Lys Ile Lys Lys Ala Cys Gly Asn Phe Gly Ile Pro Cys
115    120         125
Glu Leu Arg Val Thr Ser Ala His Lys Gly Pro Asp Glu Thr Leu Arg
130    135         140
Ile Lys Ala Glu Tyr Glu Gly Asp Gly Ile Pro Thr Val Phe Val Ala
145    150         155        160
Val Ala Gly Arg Ser Asn Gly Leu Gly Pro Val Met Ser Gly Asn Thr
165    170         175
Ala Tyr Pro Val Ile Ser Cys Pro Pro Leu Thr Pro Asp Trp Gly Val
180    185         190
Gln Asp Val Trp Ser Ser Leu Arg Leu Pro Ser Gly Leu Gly Cys Ser
195    200         205
Thr Val Leu Ser Pro Glu Gly Ser Ala Gln Phe Ala Ala Gln Ile Phe
210    215         220
Gly Leu Ser Asn His Leu Val Trp Ser Lys Leu Arg Ala Ser Ile Leu
225    230         235        240
Asn Thr Trp Ile Ser Leu Lys Gln Ala Asp Lys Lys Ile Arg Glu Cys
245    250         255
Asn Leu

```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1038 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```

Ile Gln Arg Phe Gly Thr Ser Gly His Ile Met Asn Leu Gln Ala Gln
 1      5          10        15

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Pro Lys Ala Gln Asn Lys Arg Lys Arg Cys Leu Phe Gly Gly Gln Glu
 20 25 30
 Pro Ala Pro Lys Glu Gln Pro Pro Pro Leu Gln Pro Pro Gln Gln Ser
 35 40 45
 Ile Arg Val Lys Glu Glu Gln Tyr Leu Gly His Glu Gly Pro Gly Gly
 50 55 60
 Ala Val Ser Thr Ser Gln Pro Val Glu Leu Pro Pro Pro Ser Ser Leu
 65 70 75 80
 Ala Leu Leu Asn Ser Val Val Tyr Gly Pro Glu Arg Thr Ser Ala Ala
 85 90 95
 Met Leu Ser Gln Gln Val Ala Ser Val Lys Trp Pro Asn Ser Val Met
 100 105 110
 Ala Pro Gly Arg Gly Pro Glu Arg Gly Gly Gly Val Ser Asp
 115 120 125
 Ser Ser Trp Gln Gln Pro Gly Gln Pro Pro Pro His Ser Thr Trp
 130 135 140
 Asn Cys His Ser Leu Ser Leu Tyr Ser Ala Thr Lys Gly Ser Pro His
 145 150 155 160
 Pro Gly Val Gly Val Pro Thr Tyr Tyr Asn His Pro Glu Ala Leu Lys
 165 170 175
 Arg Glu Lys Ala Gly Gly Pro Gln Leu Asp Arg Tyr Val Arg Pro Met
 180 185 190
 Met Pro Gln Lys Val Gln Leu Glu Val Gly Arg Pro Gln Ala Pro Leu
 195 200 205
 Asn Ser Phe His Ala Ala Lys Lys Pro Pro Asn Gln Ser Leu Pro Leu
 210 215 220
 Gln Pro Phe Gln Leu Ala Phe Gly His Gln Val Asn Arg Gln Val Phe
 225 230 235 240
 Arg Gln Gly Pro Pro Pro Asn Pro Val Ala Ala Phe Pro Pro Gln
 245 250 255
 Lys Gln Gln Gln Gln Gln Pro Gln Gln Gln Gln Gln Gln Gln
 260 265 270
 Ala Ala Leu Pro Gln Met Pro Leu Phe Glu Asn Phe Tyr Ser Met Pro
 275 280 285
 Gln Gln Pro Ser Gln Gln Pro Gln Asp Phe Gly Leu Gln Pro Ala Gly
 290 295 300
 Pro Leu Gly Gln Ser His Leu Ala His His Ser Met Ala Pro Tyr Pro
 305 310 315 320
 Phe Pro Pro Asn Pro Asp Met Asn Pro Glu Leu Arg Lys Ala Leu Leu
 325 330 335
 Gln Asp Ser Ala Pro Gln Pro Ala Leu Pro Gln Val Gln Ile Pro Phe
 340 345 350
 Pro Arg Arg Ser Arg Arg Leu Ser Lys Glu Gly Ile Leu Pro Pro Ser
 355 360 365
 Ala Leu Asp Gly Ala Gly Thr Gln Pro Gly Gln Glu Ala Thr Gly Asn
 370 375 380
 Leu Phe Leu His His Trp Pro Leu Gln Gln Pro Pro Pro Gly Ser Leu
 385 390 395 400
 Gly Gln Pro His Pro Glu Ala Leu Gly Phe Pro Leu Glu Leu Arg Glu
 405 410 415
 Ser Gln Leu Leu Pro Asp Gly Glu Arg Leu Ala Pro Asn Gly Arg Glu
 420 425 430
 Arg Glu Ala Pro Ala Met Gly Ser Glu Glu Gly Met Arg Ala Val Ser
 435 440 445
 Thr Gly Asp Cys Gly Gln Val Leu Arg Gly Gly Val Ile Gln Ser Thr
 450 455 460
 Arg Arg Arg Arg Ala Ser Gln Glu Ala Asn Leu Leu Thr Leu Ala
 465 470 475 480
 Gln Lys Ala Val Glu Leu Ala Ser Leu Gln Asn Ala Lys Asp Gly Ser
 485 490 495
 Gly Ser Glu Glu Lys Arg Lys Ser Val Leu Ala Ser Thr Thr Lys Cys
 500 505 510
 Gly Val Glu Phe Ser Glu Pro Ser Leu Ala Thr Lys Arg Ala Arg Glu
 515 520 525
 Asp Ser Gly Met Val Pro Leu Ile Ile Pro Val Ser Val Pro Val Arg
 530 535 540
 Thr Val Asp Pro Thr Glu Ala Ala Gln Ala Gly Gly Leu Asp Glu Asp
 545 550 555 560
 Gly Lys Gly Leu Glu Gln Asn Pro Ala Glu His Lys Pro Ser Val Ile
 565 570 575
 Val Thr Arg Arg Arg Ser Thr Arg Ile Pro Gly Thr Asp Ala Gln Ala
 580 585 590
 Gln Ala Glu Asp Met Asn Val Lys Leu Glu Gly Glu Pro Ser Val Arg

595	600	605
Lys Pro Lys Gln Arg Pro Arg Pro Glu Pro Leu Ile Ile Pro Thr Lys		
610	615	620
Ala Gly Thr Phe Ile Ala Pro Pro Val Tyr Ser Asn Ile Thr Pro Tyr		
625	630	635
Gln Ser His Leu Arg Ser Pro Val Arg Leu Ala Asp His Pro Ser Glu		
645	650	655
Arg Ser Phe Glu Leu Pro Pro Tyr Thr Pro Pro Pro Ile Leu Ser Pro		
660	665	670
Val Arg Glu Gly Ser Gly Leu Tyr Phe Asn Ala Ile Ile Ser Thr Ser		
675	680	685
Thr Ile Pro Ala Pro Pro Ile Thr Pro Lys Ser Ala His Arg Thr		
690	695	700
Leu Leu Arg Thr Asn Ser Ala Glu Val Thr Pro Pro Val Leu Ser Val		
705	710	715
Met Gly Glu Ala Thr Pro Val Ser Ile Glu Pro Arg Ile Asn Val Gly		
725	730	735
Ser Arg Phe Gln Ala Glu Ile Pro Leu Met Arg Asp Arg Ala Leu Ala		
740	745	750
Ala Ala Asp Pro His Lys Ala Asp Leu Val Trp Gln Pro Trp Glu Asp		
755	760	765
Leu Glu Ser Ser Arg Glu Lys Gln Arg Gln Val Glu Asp Leu Leu Thr		
770	775	780
Ala Ala Cys Ser Ser Ile Phe Pro Gly Ala Gly Thr Asn Gln Glu Leu		
785	790	795
Ala Leu His Cys Leu His Glu Ser Arg Gly Asp Ile Leu Glu Thr Leu		
805	810	815
Asn Lys Leu Leu Lys Lys Pro Leu Arg Pro His Asn His Pro Leu		
820	825	830
Ala Thr Tyr His Tyr Thr Gly Ser Asp Gln Trp Lys Met Ala Glu Arg		
835	840	845
Lys Leu Phe Asn Lys Gly Ile Ala Ile Tyr Lys Lys Asp Phe Phe Leu		
850	855	860
Val Gln Lys Leu Ile Gln Thr Lys Thr Val Ala Gln Cys Val Glu Phe		
865	870	875
Tyr Tyr Thr Tyr Lys Lys Gln Val Lys Ile Gly Arg Asn Gly Thr Leu		
885	890	895
Thr Phe Gly Asp Val Asp Thr Ser Asp Glu Lys Ser Ala Gln Glu Glu		
900	905	910
Val Glu Val Asp Ile Lys Thr Ser Gln Lys Phe Pro Arg Val Pro Leu		
915	920	925
Pro Arg Arg Glu Ser Pro Ser Glu Glu Arg Leu Glu Pro Lys Arg Glu		
930	935	940
Val Lys Glu Pro Arg Lys Glu Gly Glu Glu Glu Val Pro Glu Ile Gln		
945	950	955
Glu Lys Glu Glu Gln Glu Glu Gly Arg Glu Arg Ser Arg Arg Ala Ala		
965	970	975
Ala Val Lys Ala Thr Gln Thr Leu Gln Ala Asn Glu Ser Ala Ser Asp		
980	985	990
Ile Leu Ile Leu Arg Ser His Glu Ser Asn Ala Pro Gly Ser Ala Gly		
995	1000	1005
Gly Gln Ala Ser Glu Lys Pro Arg Glu Gly Thr Gly Lys Ser Arg Arg		
1010	1015	1020
Ala Leu Pro Phe Ser Glu Lys Lys Lys Lys Gln Lys Ala		
1025	1030	1035

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Ile Arg His Glu Val Ser Phe Leu Trp Asn Thr Glu Ala Ala Cys Pro		
1	5	10
Ile Gln Thr Thr Thr Asp Thr Asp Gln Ala Cys Ser Ile Arg Asp Pro		
20	25	30
Asn Ser Gly Phe Val Phe Asn Leu Asn Pro Leu Asn Ser Ser Gln Gly		
35	40	45

Tyr Asn Val Ser Gly Ile Gly Lys Ile Phe Met Phe Asn Val Cys Gly
50 55 60
Thr Met Pro Val Cys Gly Thr Ile Leu Gly Lys Pro Ala Ser Gly Cys
65 70 75 80
Glu Ala Glu Thr Gln Thr Glu Glu Leu Lys Asn Trp Lys Pro Ala Arg
85 90 95
Pro Val Gly Ile Glu Lys Ser Leu Gln Leu Ser Thr Glu Gly Phe Ile
100 105 110
Thr Leu Thr Tyr Lys Gly Pro Leu Ser Ala Lys Gly Thr Ala Asp Ala
115 120 125
Phe Ile Val Arg Phe Val Cys Asn Asp Asp Val Tyr Ser Gly Pro Leu
130 135 140
Lys Phe Leu His Gln Asp Ile Asp Ser Gly Gln Gly Ile Arg Asn Thr
145 150 155 160
Tyr Phe Glu Phe Glu Thr Ala Leu Ala Cys Val Pro Ser Pro Val Asp
165 170 175
Cys Gln Val Thr Asp Leu Ala Gly Asn Glu Tyr Asp Leu Thr Gly Leu
180 185 190
Ser Thr Val Arg Lys Pro Trp Thr Ala Val Asp Thr Ser Val Asp Gly
195 200 205
Arg Lys Arg Thr Phe Tyr Leu Ser Val Cys Asn Pro Leu Pro Tyr Ile
210 215 220
Pro Gly Cys Gln Gly Ser Ala Val Gly Ser Cys Leu Val Ser Glu Gly
225 230 235 240
Asn Ser Trp Asn Leu Gly Val Val Gln Met Ser Pro Gln Ala Ala Ala
245 250 255
Asn Gly Ser Leu Ser Ile Met Tyr Val Asn Gly Asp Lys Cys Gly Asn
260 265 270
Gln Arg Phe Ser Thr Arg Ile Thr Phe Glu Cys Ala Gln Ile Ser Gly
275 280 285
Ser Pro Ala Phe Gln Leu Gln Asp Gly Cys Glu Tyr Val Phe Ile Trp
290 295 300
Arg Thr Val Glu Ala Cys Pro Val Val Arg Val Glu Gly Asp Asn Cys
305 310 315 320
Glu Val Lys Asp Pro Arg His Gly Asn Leu Tyr Asp Leu Lys Pro Leu
325 330 335
Gly Leu Asn Asp Thr Ile Val Ser Ala Gly Glu Tyr Thr Tyr Tyr Phe
340 345 350
Arg Val Cys Gly Lys Leu Ser Ser Asp Val Cys Pro Thr Ser Asp Lys
355 360 365
Ser Lys Val Val Ser Ser Cys Gln Glu Lys Arg Glu Pro Gln Gly Phe
370 375 380
His Lys Val Ala Gly Leu Leu Thr Gln Lys Leu Thr Tyr Glu Asn Gly
385 390 395 400
Leu Leu Lys Met Asn Phe Thr Gly Gly Asp Thr Cys His Lys Val Tyr
405 410 415
Gln Arg Ser Thr Ala Ile Phe Phe Tyr Cys Asp Arg Gly Thr Gln Arg
420 425 430
Pro Val Phe Leu Lys Glu Thr Ser Asp Cys Ser Tyr Leu Phe Glu Trp
435 440 445
Arg Thr Gln Tyr Ala Cys Pro Pro Phe Asp Leu Thr Glu Cys Ser Phe
450 455 460
Lys Asp Gly Ala Gly Asn Ser Phe Asp Leu Ser Ser Leu Ser Arg Tyr
465 470 475 480
Ser Asp Asn Trp Glu Ala Ile Thr Gly Thr Gly Asp Pro Glu His Tyr
485 490 495
Leu Ile Asn Val Cys Lys Ser Leu Ala Gly Thr Glu Pro
500 505 510
Cys Pro Pro Glu Ala Ala Ala Cys Leu Leu Gly Gly Ser Lys Pro Val
515 520 525
Asn Leu Gly Arg Val Arg Asp Gly Pro Gln Trp Arg Asp Gly Ile Ile
530 535 540
Val Leu Lys Tyr Val Asp Gly Asp Leu Cys Pro Asp Gly Ile Arg Lys
545 550 555 560
Lys Ser Thr Thr Ile Arg Phe Thr Cys Ser Glu Ser Gln Val Asn Ser
565 570 575
Arg Pro Met Phe Ile Ser Ala Val Glu Asp Cys Glu Tyr Thr Phe Ala
580 585 590
Trp Pro Thr Ala Thr Ala Cys Pro Met Lys Ser Asn Glu His Asp Asp
595 600 605
Cys Gln Val Thr Asn Pro Ser Thr Gly His Leu Phe Asp Leu Ser Ser
610 615 620
Leu Ser Gly Arg Ala Gly Phe Thr Ala Ala Tyr Ser Glu Lys Gly Leu

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met Ala Arg Leu Ser Arg Pro Glu Arg Pro Asp Leu Val Phe Glu Glu
 1 5 10 15
 Glu Asp Leu Pro Tyr Glu Glu Glu Ile Met Arg Asn Gln Phe Ser Val
 20 25 30
 Lys Cys Trp Leu His Tyr Ile Glu Phe Lys Gln Gly Ala Pro Lys Pro
 35 40 45
 Arg Leu Asn Gln Leu Tyr Glu Arg Ala Leu Lys Leu Leu Pro Cys Ser
 50 55 60
 Tyr Lys Leu Trp Tyr Arg Tyr Leu Lys Ala Arg Arg Ala Gln Val Lys
 65 70 75 80
 His Arg Cys Val Thr Asp Pro Ala Tyr Glu Asp Val Asn Asn Cys His
 85 90 95
 Glu Arg Ala Phe Val Phe Met His Lys Met Pro Arg Leu Trp Leu Asp
 100 105 110
 Tyr Cys Gln Phe Leu Met Asp Gln Gly Arg Val Thr His Thr Arg Arg
 115 120 125
 Thr Phe Asp Arg Ala Leu Arg Ala Leu Pro Ile Thr Gln His Ser Arg
 130 135 140
 Ile Trp Pro Leu Tyr Leu Arg Phe Leu Arg Ser His Pro Leu Pro Glu
 145 150 155 160
 Thr Ala Val Arg Gly Tyr Arg Arg Phe Leu Lys Leu Ser Pro Glu Ser
 165 170 175
 Ala Glu Glu Tyr Ile Glu Tyr Leu Lys Ser Ser Asp Arg Leu Asp Glu
 180 185 190
 Ala Ala Gln Arg Leu Ala Thr Val Val Asn Asp Glu Arg Phe Val Ser
 195 200 205
 Lys Ala Gly Lys Ser Asn Tyr Gln Leu Trp His Glu Leu Cys Asp Leu
 210 215 220
 Ile Ser Gln Asn Pro Asp Lys Val Gln Ser Leu Asn Val Asp Ala Ile
 225 230 235 240
 Ile Arg Gly Gly Leu Thr Arg Phe Thr Asp Gln Leu Gly Lys Leu Trp
 245 250 255

Cys Ser Leu Ala Asp Tyr Tyr Ile Arg Ser Gly His Phe Glu Lys Ala
260 265 270
Arg Asp Val Tyr Glu Glu Ala Ile Arg Thr Val Met Thr Val Arg Asp
275 280 285
Phe Thr Gln Val Phe Asp Ser Tyr Ala Gln Phe Glu Glu Ser Met Ile
290 295 300
Ala Ala Lys Met Glu Thr Ala Ser Glu Leu Gly Arg Glu Glu Glu Asp
305 310 315 320
Asp Val Asp Leu Glu Leu Arg Leu Ala Arg Phe Glu Gln Leu Ile Ser
325 330 335
Arg Arg Pro Leu Leu Leu Asn Ser Val Leu Leu Arg Gln Asn Pro His
340 345 350
His Val His Glu Trp His Lys Arg Val Ala Leu His Gln Gly Arg Pro
355 360 365
Arg Glu Ile Ile Asn Thr Tyr Glu Ala Val Gln Thr Val Asp Pro
370 375 380
Phe Lys Ala Thr Gly Lys Pro His Thr Leu Trp Val Ala Phe Ala Lys
385 390 395 400
Phe Tyr Glu Asp Asn Gly Gln Leu Asp Asp Ala Arg Val Ile Leu Glu
405 410 415
Lys Ala Thr Lys Val Asn Phe Lys Gln Val Asp Asp Leu Ala Ser Val
420 425 430
Trp Cys Gln Cys Gly Glu Leu Glu Leu Arg His Glu Asn Tyr Asp Glu
435 440 445
Ala Leu Arg Leu Leu Arg Lys Ala Thr Ala Leu Pro Ala Arg Arg Ala
450 455 460
Glu Tyr Phe Asp Gly Ser Glu Pro Val Gln Asn Arg Val Tyr Lys Ser
465 470 475 480
Leu Lys Val Trp Ser Met Leu Ala Asp Leu Glu Glu Ser Leu Gly Thr
485 490 495
Phe Gln Ser Thr Lys Ala Val Tyr Asp Arg Ile Leu Asp Leu Arg Ile
500 505 510
Ala Thr Pro Gln Ile Val Ile Asn Tyr Ala Met Phe Leu Glu Glu His
515 520 525
Lys Tyr Phe Glu Glu Ser Phe Lys Ala Tyr Glu Arg Gly Ile Ser Leu
530 535 540
Phe Lys Trp Pro Asn Val Ser Asp Ile Trp Ser Thr Tyr Leu Thr Lys
545 550 555 560
Phe Ile Ala Arg Tyr Gly Gly Arg Lys Leu Glu Arg Ala Arg Asp Leu
565 570 575
Phe Glu Gln Ala Leu Asp Gly Cys Pro Pro Lys Tyr Ala Lys Thr Leu
580 585 590
Tyr Leu Leu Tyr Ala Gln Leu Glu Glu Trp Gly Leu Ala Arg His
595 600 605
Ala Met Ala Val Tyr Glu Arg Ala Thr Arg Ala Val Glu Pro Ala Gln
610 615 620
Gln Tyr Asp Met Phe Asn Ile Tyr Ile Lys Arg Ala Ala Glu Ile Tyr
625 630 635 640
Gly Val Thr His Thr Arg Gly Ile Tyr Gln Lys Ala Ile Glu Val Leu
645 650 655
Ser Asp Glu His Ala Arg Glu Met Cys Leu Arg Phe Ala Asp Met Glu
660 665 670
Cys Lys Leu Gly Glu Ile Asp Arg Ala Arg Ala Ile Tyr Ser Phe Cys
675 680 685
Ser Gln Ile Cys Asp Pro Arg Thr Thr Gly Ala Phe Trp Gln Thr Trp
690 695 700
Lys Asp Phe Glu Val Arg His Gly Asn Glu Asp Thr Ile Lys Glu Met
705 710 715 720
Leu Arg Ile Arg Arg Ser Val Gln Ala Thr Tyr Asn Thr Gln Val Asn
725 730 735
Phe Met Ala Ser Gln Met Leu Lys Val Ser Gly Ser Ala Thr Gly Thr
740 745 750
Val Ser Asp Leu Ala Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu
755 760 765
Leu Glu Gln Arg Ala Glu Gln Leu Ala Ala Glu Ala Glu Arg Asp Gln
770 775 780
Pro Leu Arg Ala Gln Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser
785 790 795 800
Arg Glu Glu Leu Ala Glu Leu Ala Gln Gln Val Asn Pro Glu Glu Ile
805 810 815
Gln Leu Gly Glu Asp Glu Asp Glu Asp Glu Met Asp Leu Glu Pro Asn
820 825 830
Glu Val Arg Leu Glu Gln Gln Ser Val Pro Ala Ala Val Phe Gly Ser

835	840	845
Leu Lys Glu Asp		
850		

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met Phe Ser Ala Leu Lys Lys Leu Val Gly Ser Asp Gln Ala Pro Gly
 1 5 10 15
 Arg Asp Lys Asn Ile Pro Ala Gly Leu Gln Ser Met Asn Gln Ala Leu
 20 25 30
 Gln Arg Arg Phe Ala Lys Gly Val Gln Tyr Asn Met Lys Ile Val Ile
 35 40 45
 Arg Gly Asp Arg Asn Thr Gly Lys Thr Ala Leu Trp His Arg Leu Gln
 50 55 60
 Gly Arg Pro Phe Val Glu Glu Tyr Ile Pro Thr Gln Glu Ile Gln Val
 65 70 75 80
 Thr Ser Ile His Trp Ser Tyr Lys Thr Thr Asp Asp Ile Val Lys Val
 85 90 95
 Glu Val Trp Asp Val Val Asp Lys Gly Lys Cys Lys Lys Arg Gly Asp
 100 105 110
 Gly Leu Lys Met Glu Asn Asp Pro Gln Glu Xaa Glu Ser Glu Met Ala
 115 120 125
 Leu Asp Ala Glu Phe Leu Asp Val Tyr Lys Asn Cys Asn Gly Val Val
 130 135 140
 Met Met Phe Asp Ile Thr Lys Gln Trp Thr Phe Asn Tyr Ile Leu Arg
 145 150 155 160
 Glu Leu Pro Lys Val Pro Thr His Val Pro Val Cys Val Leu Gly Asn
 165 170 175
 Tyr Arg Asp Met Gly Glu His Arg Val Ile Leu Pro Asp Asp Val Arg
 180 185 190
 Asp Phe Ile Asp Asn Leu Asp Arg Pro Pro Gly Ser Ser Tyr Phe Arg
 195 200 205
 Tyr Ala Glu Ser Ser Met Lys Asn Ser Phe Gly Leu Lys Tyr Leu His
 210 215 220
 Lys Phe Phe Asn Ile Pro Phe Leu Gln Leu Gln Arg Glu Thr Leu Leu
 225 230 235 240
 Arg Gln Leu Glu Thr Asn Gln Leu Asp Met Asp Ala Thr Leu Glu Glu
 245 250 255
 Leu Ser Val Gln Gln Glu Thr Glu Asp Gln Asn Tyr Gly Ile Phe Leu
 260 265 270
 Glu Met Met Glu Ala Arg Ser Arg Gly His Ala Ser Pro Leu Ala Ala
 275 280 285
 Asn Gly Gln Ser Pro Ser Pro Gly Ser Gln Ser Pro Val Leu Pro Ala
 290 295 300
 Pro Ala Val Ser Thr Gly Ser Ser Ser Pro Gly Thr Pro Gln Pro Ala
 305 310 315 320
 Pro Gln Leu Pro Leu Asn Ala Ala Pro Pro Ser Ser Val Pro Pro Val
 325 330 335
 Pro Pro Ser Glu Ala Leu Pro Pro Ala Cys Pro Ser Ala Pro Ala
 340 345 350
 Pro Arg Arg Ser Ile Ile Ser Arg Leu Phe Gly Thr Ser Pro Ala Thr
 355 360 365
 Glu Ala Ala Pro Pro Pro Pro Glu Pro Val Pro Ala Ala Gln Gly Pro
 370 375 380
 Ala Thr Val Gln Ser Val Glu Asp Phe Val Pro Asp Asp Arg Leu Asp
 385 390 395 400
 Arg Ser Phe Leu Glu Asp Thr Thr Pro Ala Arg Asp Glu Lys Lys Val
 405 410 415
 Gly Ala Lys Ala Ala Gln Gln Asp Ser Asp Ser Asp Gly Glu Ala Leu
 420 425 430
 Gly Gly Asn Pro Met Val Ala Gly Phe Gln Asp Asp Val Asp Leu Glu
 435 440 445
 Asp Gln Pro Arg Gly Ser Pro Pro Leu Pro Ala Gly Pro Val Pro Ser
 450 455 460

Gln Asp Ile Thr Leu Ser Ser Glu Glu Glu Ala Glu Val Ala Ala Pro
465 470 475 480
Thr Lys Gly Pro Ala Pro Ala Pro Gln Gln Cys Ser Glu Pro Glu Thr
485 490 495
Lys Trp Ser Ser Ile Pro Ala Ser Lys Pro Arg Arg Gly Thr Ala Pro
500 505 510
Thr Arg Thr Ala Ala Pro Pro Itp Pro Gly Gly Val Ser Val Arg Thr
515 520 525
Gly Pro Glu Lys Arg Ser Ser Thr Arg Pro Pro Ala Glu Met Glu Pro
530 535 540
Gly Lys Gly Glu Gln Ala Ser Ser Ser Glu Ser Asp Pro Glu Gly Pro
545 550 555 560
Ile Ala Ala Gln Met Leu Ser Phe Val Met Asp Asp Pro Asp Phe Glu
565 570 575
Ser Glu Gly Ser Asp Thr Gln Arg Arg Ala Asp Asp Phe Pro Val Arg
580 585 590
Asp Asp Pro Ser Asp Val Thr Asp Glu Asp Glu Gly Pro Ala Glu Pro
595 600 605
Pro Pro Pro Pro Lys Leu Pro Leu Pro Ala Phe Arg Leu Lys Asn Asp
610 615 620
Ser Asp Leu Phe Gly Leu Gly Leu Glu Ala Gly Pro Lys Glu Ser
625 630 635 640
Ser Glu Glu Gly Lys Glu Gly Lys Thr Pro Ser Lys Glu Lys Lys Lys
645 650 655
Lys Thr Lys Ser Phe Ser Arg Val Leu Leu Glu Arg Pro Arg Ala His
660 665 670
Arg Phe Ser Thr Arg Val Gly Tyr Gln Val Ser Val Pro Asn Ser Pro
675 680 685
Tyr Ser Glu Ser Tyr
690